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PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR;  
 XX  
 XX WPI; 2001-367863/38.  
 DR  
 XX  
 PT Identifying complementary peptides by analysis of protein and  
 PT nucleotide sequence databases, useful in drug design -  
 XX  
 XX Example 5; Page 385; 488pp; English.  
 PS  
 XX The invention relates to the identification of complementary peptides  
 CC by analysis of protein and nucleotide sequence databases from higher  
 CC eukaryotic genomes, excluding human and plants. The specific  
 CC complementary peptides interact with their relevant target proteins  
 CC encoded in the eukaryote genome. The peptides may be used as reagents  
 CC and drugs for drug discovery and as lead ligands for drug design and  
 CC development. The present sequence is a complementary peptide from  
 CC Saccharomyces cerevisiae.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 20; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 DB 6 DLDA 9  
 RESULT 19  
 ID AAB46866 standard; peptide; 10 AA.  
 XX  
 AC AAB46866;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #5.  
 XX  
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
 KW cytosatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
 KW vulnary; cerebroprotective; antiangiinal; antidiabetic; nephrotropic;  
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;  
 KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5 /note= "D-form residue"  
 FT Modified-site 9 /label= Abu  
 FT /note= "2-aminobutyric acid"  
 FT Modified-site 10 /label= Abu  
 FT /note= "2-aminobutyric acid"  
 FT  
 XX  
 XX DE19933173-A1.  
 XX  
 XX 18-JAN-2001.  
 PD  
 XX  
 PF 15-JUL-1999; 99DE-1033173.  
 XX  
 PR 15-JUL-1999; 99DE-1033173.  
 XX  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Jonczyk A, Diefenbach B, Goodman S;  
 PI  
 XX

DR WPI; 2001-192448/20.  
 XX  
 PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
 PT useful e.g. for treating thrombosis, coronary heart disease, tumors,  
 PT osteoporosis, inflammation or infections -  
 XX  
 PS Claim 3; Page 5; 20pp; German.  
 XX  
 CC This invention describes novel cyclic peptides (I), containing 8 amino  
 CC acid residues and optionally further alpha,omega-aminocarboxylic acid  
 CC residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-Asp-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
 CC X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
 CC X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
 CC Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, His or  
 CC Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
 CC length of 50-2500 mm, or is absent; the amino acid residues are  
 CC optionally derivatized and include D- as well as L-forms (in the case of  
 CC optically active aminoacids). The products of the invention have  
 CC antithrombotic, cardiant, antiarteriosclerotic, cytosatic, osteopathic,  
 CC antiinflammatory, antibacterial, antipsoriatic, vulnary,  
 CC cerebroprotective, antiangiinal, antidiabetic, ophthalmological,  
 CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
 CC neuroprotective. (I) are used for treating diseases involving expression  
 CC and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
 CC wound healing deficiency. Other disclosed disorders to be treated include  
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
 CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or  
 CC rubecotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may  
 CC also be useful in analytical biology and molecular biology; e.g.  
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
 CC used to prepare affinity chromatography columns for purifying integrins.  
 CC DNA encoding (I) may be used for treating the same disorders as (I)  
 CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
 CC receptor inhibiting activity.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 20; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 DB 3 DLDA 6  
 RESULT 20  
 ID AAB46867 standard; peptide; 10 AA.  
 XX  
 AC AAB46867;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #6.  
 XX  
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
 KW cytosatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
 KW vulnary; cerebroprotective; antiangiinal; antidiabetic; nephrotropic;  
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;  
 KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 5 /note= "D-form residue"  
 FT

[illegible]



CC DNA encoding (I) may be used for treating the same disorders as (I)  
 CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
 CC receptor inhibiting activity.

XX Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

RESULT 22

AAB46885

ID AAB46885 standard; peptide; 10 AA.

XX AC AAB46885;

XX DT 09-MAY-2001 (first entry)

XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #17.

XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;

XX cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

XX vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;

XX ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

XX neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;

XX cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;

XX osteoporosis; inflammation; infection; psoriasis; wound healing.

XX OS Synthetic.

XX XX

XX FH Key Location/Qualifiers

XX Misc-difference 5

XX FT /note= "D-form residue"

XX FT

XX XX

XX PN DE19933173-Al.

XX XX

XX PD 18-JAN-2001.

XX XX

XX PF 15-JUL-1999; 99DE-1033173.

XX XX

XX PR 15-JUL-1999; 99DE-1033173.

XX XX

XX PA (MERE ) MERCK PATENT GMBH.

XX XX

XX PI Jonczyk A, Diefenbach B, Goodman S;

XX XX

XX XX WPI; 2001-192448/20.

XX XX

XX PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors

XX useful e.g. for treating thrombosis, coronary heart disease, tumors,

XX PT osteoporosis, inflammation or infections

XX XX

XX PS Example 1; Page 10; 20pp; German.

XX XX

CC This invention describes novel cyclic peptides (I), containing 8 amino

CC acid residues and optionally further alpha,omega-aminocarboxylic acid

CC residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-

CC X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;

CC X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =

CC Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or

CC Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a

CC length of 50-2500 mum; or is absent; the amino acid residues are

CC optionally derivatized and include D- as well as L-forms (in the case of

CC optically active aminoacids). The products of the invention have

CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,

CC antiinflammatory, antibacterial, antipsoriatic, vulnary,

CC cerebroprotective, antianginal, antidiabetic, ophthalmological,

CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,

CC neuroprotective. (I) are used for treating diseases involving expression  
 CC and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
 CC wound healing deficiency. Other disclosed disorders to be treated include  
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
 CC retinopathy, macular degeneration, myopia, ocular histioplasmosis or  
 CC rubebotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may  
 CC also be useful in analytical biology and molecular biology; e.g.

CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be

CC used to prepare affinity chromatography columns for purifying integrins.

CC DNA encoding (I) may be used for treating the same disorders as (I)

CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin

CC receptor inhibiting activity.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

RESULT 23

AAB46862

ID AAB46862 standard; peptide; 11 AA.

XX AC AAB46862;

XX DT 09-MAY-2001 (first entry)

XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #1.

XX XX

XX KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;

XX KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

XX KW vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;

XX KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

XX KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;

XX KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;

XX KW osteoporosis; inflammation; infection; psoriasis; wound healing.

XX OS Synthetic.

XX XX

XX FN DE19933173-Al.

XX XX

XX PD 18-JAN-2001.

XX XX

XX PF 15-JUL-1999; 99DE-1033173.

XX XX

XX PR 15-JUL-1999; 99DE-1033173.

XX XX

XX PA (MERE ) MERCK PATENT GMBH.

XX XX

XX PI Jonczyk A, Diefenbach B, Goodman S;

XX XX

XX DR WPI; 2001-192448/20.

XX XX

XX PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors

XX useful e.g. for treating thrombosis, coronary heart disease, tumors,

XX PT osteoporosis, inflammation or infections

XX XX

XX PS Claim 3; Page 5; 20pp; German.

XX XX

CC This invention describes novel cyclic peptides (I), containing 8 amino

CC acid residues and optionally further alpha,omega-aminocarboxylic acid

CC residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-

CC X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;

CC X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =

CC Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =

CC Gly, Ala or Ser; X\_5 = Leu, Ile, Nle, Val or Phe; X\_6 = Arg, Har or  
 CC Lys; R\_1 = one or more omega-aminocarboxylic acid residues, having a  
 CC length of 50-2500 mm; or is absent; the amino acid residues are  
 CC optionally derivatized and include D- as well as L-forms (in the case of  
 CC optically active aminoacids). The products of the invention have  
 CC antithrombotic, cardiant, antiarteriosclerotic, cytotatic, osteopathic,  
 CC antiinflammatory, antibacterial, antipsoriatic, vulnary,  
 CC cerebroprotective, antianginal, antidiabetic, ophthalmological,  
 CC antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic,  
 CC neuroprotective. (I) are used for treating diseases involving expression  
 CC and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
 CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
 CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
 CC wound healing deficiency. Other disclosed disorders to be treated include  
 CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
 CC retinopathy, macular degeneration, myopia, ocular histioplasmosis or  
 CC rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
 CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
 CC acute renal failure, renal inflammation or multiple sclerosis. (I) may  
 CC also be useful in analytical biology and molecular biology; e.g.  
 CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
 CC used to prepare affinity chromatography columns for purifying integrins.  
 CC DNA encoding (I) may be used for treating the same disorders as (I)  
 CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
 CC receptor inhibiting activity.  
 CC  
 CC SQ Sequence 11 AA;  
 Query Match 100.0%; Score 20; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 Db ||||  
 3 DLDA 6  
 RESULT 24  
 AAB46865  
 ID AAB46865 standard; peptide; 11 AA.  
 XX  
 AC AAB46865;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #4.  
 XX  
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
 KW cytotatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
 KW vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;  
 KW ophthalmological; antiarthritic; antirheumatic; antitumor; vasotropic;  
 KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 5 /note= "D-form residue"  
 FT  
 XX  
 PN DE19933173-Al.  
 XX  
 XX 18-JAN-2001.  
 XX  
 XX 15-JUL-1999; 99DE-1033173.  
 XX  
 XX 15-JUL-1999; 99DE-1033173.  
 XX  
 XX (MERE ) MERCK PATENT GMBH.  
 XX  
 XX Jonczyk A, Diefenbach B, Goodman S;  
 PI  
 XX 18-JAN-2001.

WPI; 2001-192448/20.

New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors useful e.g. for treating thrombosis, coronary heart disease, tumors, osteoporosis, inflammation or infections -  
 Claim 3; Page 5; 20pp; German.

This invention describes novel cyclic peptides (I), containing 8 amino acid residues and optionally further alpha,omega-aminocarboxylic acid residues. Cyclic peptides of formula Cyclo-(Arg-X\_1-X\_2-X\_3-X\_4-X\_5-X\_6-R\_1) (I) and their salts and solvates. X\_1 = Ser, Gly or Thr; X\_2 = Leu, Ile, Nle, Val or Phe; X\_3 = Asp, Glu, Lys or Phe; X\_4 = Gly, Ala or Ser; X\_5 = Leu, Ile, Nle, Val or Phe; X\_6 = Arg, Har or Lys; R\_1 = one or more omega-aminocarboxylic acid residues, having a length of 50-2500 mm; or is absent; the amino acid residues are optionally derivatized and include D- as well as L-forms (in the case of optically active aminoacids). The products of the invention have antithrombotic, cardiant, antiarteriosclerotic, cytotatic, osteopathic, antiinflammatory, antibacterial, antipsoriatic, vulnary, cerebroprotective, antianginal, antidiabetic, ophthalmological, antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic, neuroprotective. (I) are used for treating diseases involving expression and pathological function of alpha\_vbeta\_6-integrin receptors, especially thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis, tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and wound healing deficiency. Other disclosed disorders to be treated include apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic retinopathy, macular degeneration, myopia, ocular histioplasmosis or rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty, acute renal failure, renal inflammation or multiple sclerosis. (I) may also be useful in analytical biology and molecular biology; e.g. fluorescently labeled (I) may be used as diagnostic markers or (I) may be used to prepare affinity chromatography columns for purifying integrins. DNA encoding (I) may be used for treating the same disorders as (I) itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin receptor inhibiting activity.

SQ Sequence 11 AA;

Query Match 100.0%; Score 20; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

Db ||||

3 DLDA 6

RESULT 25  
 AAB46875

ID AAB46875 standard; peptide; 11 AA.

XX  
 AC AAB46875;

XX  
 DT 09-MAY-2001 (first entry)

XX  
 DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor SEQ ID 3.

XX  
 KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
 KW cytotatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
 KW vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;  
 KW ophthalmological; antiarthritic; antirheumatic; antitumor; vasotropic;  
 KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.

XX  
 OS Synthetic.

XX  
 DE19933173-Al.

XX  
 18-JAN-2001.

XX 15-JUL-1999; 99DE-1033173.  
 XX 15-JUL-1999; 99DE-1033173.  
 XX (MERE ) MERCK PATENT GMBH.  
 XX Jonczyk A, Diefenbach B, Goodman S;  
 XX WPI; 2001-192448/20.  
 XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
 XX useful e.g. for treating thrombosis, coronary heart disease, tumors,  
 XX osteoporosis, inflammation or infections  
 XX Examples; Page 16; 20pp; German.  
 XX This invention describes novel cyclic peptides (I), containing 8 amino  
 XX acid residues and optionally further alpha,omega-aminocarboxylic acid  
 XX residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
 XX X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
 XX X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
 XX Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
 XX Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
 XX length of 50-2500 mum; or is absent; the amino acid residues are  
 XX optionally derivatized and include D- as well as L-forms (in the case of  
 XX optically active aminoacids). The products of the invention have  
 XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
 XX antiinflammatory, antibacterial, antiarteriosclerotic, vasotrophic,  
 XX cerebroprotective, antianginal, antidiabetic, ophthalmological,  
 XX antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
 XX neuroprotective. (I) are used for treating diseases involving expression  
 XX and pathological function of alpha<sub>v</sub>beta<sub>6</sub>-integrin receptors, especially  
 XX thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
 XX tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
 XX wound healing deficiency. Other disclosed disorders to be treated include  
 XX apoplexy, angina pectoris, rheumatoid arthritis, osteoarthritis, ulcerative  
 XX retinopathy, macular degeneration, myopia, ocular histioplasmosis or  
 XX colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
 XX acute renal failure, renal inflammation or multiple sclerosis. (I) may  
 XX also be useful in analytical biology and molecular biology; e.g.  
 XX fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
 XX used to prepare affinity chromatography columns for purifying integrins.  
 XX DNA encoding (I) may be used for treating the same disorders as (I)  
 XX itself. (I) are well tolerated and have good alpha<sub>v</sub>beta<sub>6</sub>-integrin  
 XX receptor inhibiting activity.  
 XX Sequence 11 AA;  
 SQ Query Match 100.0%; Score 20; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 Db 3 DLDA 6  
 RESULT 26  
 AAB46878  
 ID AAB46878 standard; peptide; 11 AA.  
 XX AAB46878;  
 AC  
 XX 09-MAY-2001 (first entry)  
 DT  
 XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor SEQ ID 6.  
 DE  
 XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
 KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
 KW vulnerary; cerebroprotective; antianginal; antidiabetic; nephrotropic;  
 KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;

KW neuroprotective; alpha<sub>v</sub>beta<sub>6</sub>-integrin receptor; thrombosis; tumor;  
 KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
 KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
 XX Synthetic.  
 OS DEL9933173-AL.  
 XX  
 PN 18-JAN-2001.  
 PD  
 XX  
 XX 15-JUL-1999; 99DE-1033173.  
 PF  
 XX  
 XX 15-JUL-1999; 99DE-1033173.  
 PR  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Jonczyk A, Diefenbach B, Goodman S;  
 PI WPI; 2001-192448/20.  
 DR New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
 XX useful e.g. for treating thrombosis, coronary heart disease, tumors,  
 XX osteoporosis, inflammation or infections  
 XX Examples; Page 17; 20pp; German.  
 XX This invention describes novel cyclic peptides (I), containing 8 amino  
 XX acid residues and optionally further alpha,omega-aminocarboxylic acid  
 XX residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
 XX X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
 XX X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
 XX Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
 XX Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
 XX length of 50-2500 mum; or is absent; the amino acid residues are  
 XX optionally derivatized and include D- as well as L-forms (in the case of  
 XX optically active aminoacids). The products of the invention have  
 XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
 XX antiinflammatory, antibacterial, antiarteriosclerotic, vasotrophic,  
 XX cerebroprotective, antianginal, antidiabetic, ophthalmological,  
 XX antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
 XX neuroprotective. (I) are used for treating diseases involving expression  
 XX and pathological function of alpha<sub>v</sub>beta<sub>6</sub>-integrin receptors, especially  
 XX thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
 XX tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
 XX wound healing deficiency. Other disclosed disorders to be treated include  
 XX apoplexy, angina pectoris, rheumatoid arthritis, osteoarthritis, ulcerative  
 XX retinopathy, macular degeneration, myopia, ocular histioplasmosis or  
 XX colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
 XX acute renal failure, renal inflammation or multiple sclerosis. (I) may  
 XX also be useful in analytical biology and molecular biology; e.g.  
 XX fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
 XX used to prepare affinity chromatography columns for purifying integrins.  
 XX DNA encoding (I) may be used for treating the same disorders as (I)  
 XX itself. (I) are well tolerated and have good alpha<sub>v</sub>beta<sub>6</sub>-integrin  
 XX receptor inhibiting activity.  
 XX Sequence 11 AA;  
 SQ Query Match 100.0%; Score 20; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 Db 3 DLDA 6  
 RESULT 27  
 AAB46887  
 ID AAB46887 standard; peptide; 11 AA.  
 XX AAB46887;  
 AC

XX 09-MAY-2001 (first entry)  
XX Integrin alpha-Vbeta-6 cyclic peptide inhibitor #19.  
XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
KW vulnary; cerebroprotective; antiangular; antidiabetic; nephrotropic;  
KW ophthalmologic; antiarthritic; antirheumatic; antiulcer; vasotropic;  
KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 5 /note= "D-form residue"  
FT  
FT  
XX DE19933173-AL.  
XX 18-JAN-2001.  
XX 15-JUL-1999; 99DE-1033173.  
XX 15-JUL-1999; 99DE-1033173.  
XX (MERE ) MERCK PATENT GMBH.  
XX Joneczyk A, Diefenbach B, Goodman S;  
XX WPI; 2001-192448/20.  
XX  
XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
XX useful e.g. for treating thrombosis, coronary heart disease, tumors,  
XX osteoporosis, inflammation or infections  
XX Example 1; Page 11; 20pp; German.  
XX  
XX This invention describes novel cyclic peptides (I), containing 8 amino  
XX acid residues and optionally further alpha,omega-aminocarboxylic acid  
XX residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-Asp-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
XX X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
XX X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
XX Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
XX Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
XX length of 50-2500 mum; or is absent; the amino acid residues are  
XX optionally derivatized and include D- as well as L-forms (in the case of  
XX optically active aminoacids). The products of the invention have  
XX antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
XX antiinflammatory, antibacterial, antipsoriatic, vulnary,  
XX cerebroprotective, antiangular, antidiabetic, ophthalmological,  
XX antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
XX neuroprotective. (I) are used for treating diseases involving expression  
XX and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
XX thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
XX tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
XX wound healing deficiency. Other disclosed disorders to be treated include  
XX apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
XX rubroretic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
XX colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
XX acute renal failure, renal inflammation or multiple sclerosis. (I) may  
XX also be useful in analytical biology and molecular biology; e.g.  
XX fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
XX used to prepare affinity chromatography columns for purifying integrins.  
XX DNA encoding (I) may be used for treating the same disorders as (I)  
XX itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
XX receptor inhibiting activity.  
XX Sequence 11 AA;

Query Match 100.0%; Score 20; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
DB 3 DLDA 6  
RESULT 28  
AAR97407  
ID AAR97407 standard; peptide; 12 AA.  
XX  
AC AAR97407;  
DT 02-DEC-1996 (first entry)  
XX  
DE Streptococcal M protein peptide, p145, fragment J(1)1.  
XX  
KW Streptococcal; M protein; peptide; p145; chimeric; chimeric;  
KW B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;  
KW detection; mapping; opsonic antibody; vaccine;  
KW group A Streptococci; immunotherapy; diagnosis.  
XX  
OS Streptococcus spp.  
XX  
XX WO9611944-A1.  
XX  
XX 25-APR-1996.  
XX  
XX 16-OCT-1995; 95WO-AU00681.  
XX  
XX 14-OCT-1994; 94AU-0008851.  
XX  
XX (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX (COUN ) COUNCIL QUEENSLAND INST MEDICAL RES.  
XX (CSLC-) CSL LTD.  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX (UYME ) UNIV MELBOURNE.  
XX  
XX Cooper JA, Good MF, Relf WA, Saul AJ;  
XX WPI; 1996-221939/22.  
XX  
XX New chimaeric peptide(s) including a conformational epitope -  
XX inserted into a peptide having similar native conformation, useful  
XX in vaccines and for determin. of minimal epitope(s) or for mapping  
XX amphipathic helices  
XX Example 13; Page 37; 99pp; English.  
XX  
XX The present peptide is a fragment of the streptococcal M protein  
XX peptide p145 (Pruksakorn et al, J. Immunol. 149: 2739-2735 (1992)),  
XX used in the construction of a novel chimaeric peptide (CP). The CP  
XX comprises a B-cell conformational epitope from within p145,  
XX inserted into a 2nd peptide, pref. an alpha-helical coil based on  
XX the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a  
XX similar conformation, enabling the epitope to be presented in an  
XX immunologically active conformation.  
XX The CP can be used in a novel detection/mapping process, e.g. to  
XX determine the min. epitope required to induce opsonic antibodies  
XX (Ab), and in vaccines against gp. A Streptococci. Ab raised against  
XX the CP can be used for immunotherapy and diagnosis, while the CP  
XX can be used diagnostically to detect Ab.  
XX  
XX Sequence 12 AA;  
XX  
XX Query Match 100.0%; Score 20; DB 17; Length 12;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
DB 3 DLDA 6

```

Db      4 DLDA 7

RESULT 29
AAR97408
ID      AAR97408 standard; peptide; 12 AA.
XX
AC      AAR97408;
XX
XX      02-DEC-1996 (first entry)
XX
DE      Streptococcal M protein peptide, p145, fragment J(I)2.
XX
KW      Streptococcal; M protein; peptide; p145; chimaeric; chimeric;
KW      B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW      detection; mapping; opsonic antibody; vaccine;
KW      group A Streptococci; immunotherapy; diagnosis.
XX
OS      Streptococcus spp.
XX
PN      WO9611944-A1.
XX
PD      25-APR-1996.
XX
PF      16-OCT-1995; 95WO-AU00681.
XX
PR      14-OCT-1994; 94AU-0008851.
XX
PA      (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA      (CSLC-) CSL LTD.
PA      (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA      (UYME ) UNIV MELBOURNE.
XX
PI      Cooper JA, Good MF, Relf WA, Saul AJ;
XX
XX      WPI; 1996-221939/22.
XX
PT      New chimaeric peptide(s) including a conformational epitope -
PT      inserted into a peptide having similar native conformation, useful
PT      in vaccines and for determin. of minimal epitope(s) or for mapping
PT      amphipathic helices
XX
XX      Example 13; Page 37; 99pp; English.
XX
CC      The present peptide is a fragment of the Streptococcal M protein
CC      peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),
CC      used in the construction of a novel chimaeric peptide (CP). The CP
CC      comprises a B-cell conformational epitope from within p145,
CC      inserted into a 2nd peptide, pref. an alpha-helical coil based on
CC      the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
CC      similar conformation, enabling the epitope to be presented in an
CC      immunologically active conformation.
CC      The CP can be used in a novel detection/mapping process, e.g. to
CC      determine the min. epitope required to induce opsonic antibodies
CC      (Ab), and in vaccines against gp. A Streptococci. Ab raised against
CC      the CP can be used for immunotherapy and diagnosis, while the CP
CC      can be used diagnostically to detect Ab.
XX
SQ      Sequence 12 AA;

Query Match      100.0%; Score 20; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DLDA 4
        ||||
Db      3 DLDA 6

RESULT 30
AAR97409
ID      AAR97409 standard; peptide; 12 AA.
XX
AC      AAR97409;
XX
XX      02-DEC-1996 (first entry)
XX
DE      Streptococcal M protein peptide, p145, fragment J(I)3.
XX
KW      Streptococcal; M protein; peptide; p145; chimaeric; chimeric;
KW      B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;
KW      detection; mapping; opsonic antibody; vaccine;
KW      group A Streptococci; immunotherapy; diagnosis.
XX
OS      Streptococcus spp.
XX
PN      WO9611944-A1.
XX
PD      25-APR-1996.
XX
PF      16-OCT-1995; 95WO-AU00681.
XX
PR      14-OCT-1994; 94AU-0008851.
XX
PA      (BIOT-) BIOTECH AUSTRALIA PTY LTD.
PA      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA      (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA      (CSLC-) CSL LTD.
PA      (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
PA      (UYME ) UNIV MELBOURNE.
XX
PI      Cooper JA, Good MF, Relf WA, Saul AJ;
XX
XX      WPI; 1996-221939/22.
XX
PT      New chimaeric peptide(s) including a conformational epitope -
PT      inserted into a peptide having similar native conformation, useful
PT      in vaccines and for determin. of minimal epitope(s) or for mapping
PT      amphipathic helices
XX
XX      Example 13; Page 37; 99pp; English.
XX
CC      The present peptide is a fragment of the Streptococcal M protein
CC      peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),
CC      used in the construction of a novel chimaeric peptide (CP). The CP
CC      comprises a B-cell conformational epitope from within p145,
CC      inserted into a 2nd peptide, pref. an alpha-helical coil based on
CC      the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a
CC      similar conformation, enabling the epitope to be presented in an
CC      immunologically active conformation.
CC      The CP can be used in a novel detection/mapping process, e.g. to
CC      determine the min. epitope required to induce opsonic antibodies
CC      (Ab), and in vaccines against gp. A Streptococci. Ab raised against
CC      the CP can be used for immunotherapy and diagnosis, while the CP
CC      can be used diagnostically to detect Ab.
XX
SQ      Sequence 12 AA;

Query Match      100.0%; Score 20; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DLDA 4
        ||||
Db      3 DLDA 6

RESULT 31
AAR97410
ID      AAR97410 standard; peptide; 12 AA.
XX
AC      AAR97410;
XX
XX      02-DEC-1996 (first entry)
XX

```

XX DE Streptococcal M protein peptide, p145, fragment J(I)4.  
XX KW Streptococcal; M protein; peptide; p145; chimeric; chimeric;  
KW B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper;  
KW detection; mapping; opsonic antibody; vaccine;  
KW group A Streptococci; immunotherapy; diagnosis.  
XX OS Streptococcus spp.  
XX XX  
XX PN WO9611944-A1.  
XX XX  
XX PD 25-APR-1996.  
XX XX  
XX PF 16-OCT-1995; 95WO-AU00681.  
XX XX  
XX PR 14-OCT-1994; 94AU-0008851.  
XX XX  
XX PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.  
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
XX PA (CSLC-) CSL LTD.  
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX PA (UYME) UNIV MELBOURNE.  
XX PI  
XX PI Cooper JA, Good MF, Relf WA, Saul AJ;  
XX WPI; 1996-221939/22.  
XX XX  
XX PT New chimeric peptide(s) including a conformational epitope -  
XX PT inserted into a peptide having similar native conformation, useful  
XX PT in vaccines and for determin. of minimal epitope(s) or for mapping  
XX PT amphipathic helices  
XX XX  
XX PS Example 13; Page 37; 99pp; English.  
XX XX  
XX CC The present peptide is a fragment of the Streptococcal M protein  
XX CC peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735 (1992)),  
XX CC used in the construction of a novel chimeric peptide (CP). The CP  
XX CC comprises a B-cell conformational epitope from within p145,  
XX CC inserted into a 2nd peptide, pref. an alpha-helical coil based on  
XX CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a  
XX CC similar conformation, enabling the epitope to be presented in an  
XX CC immunologically active conformation.  
XX CC The CP can be used in a novel detection/mapping process, e.g. to  
XX CC determine the min. epitope required to induce opsonic antibodies  
XX CC (Ab), and in vaccines against gp. A Streptococci. Ab raised against  
XX CC the CP can be used for immunotherapy and diagnosis, while the CP  
XX CC can be used diagnostically to detect Ab.  
XX XX  
XX SQ Sequence 12 AA;  
  
Query Match 100.0%; Score 20; DB 17; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
      ||||  
Db 1 DLDA 4  
  
RESULT 32  
AAB46888  
ID AAB46888 standard; peptide; 12 AA.  
XX AC AAB46888;  
XX XX  
XX DT 09-MAY-2001 (first entry)  
XX XX  
XX DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #20.  
XX KW Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
KW cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;

KW vulnery; cerebroprotective; antianigmal; antidiabetic; nephrotropic;  
KW ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;  
KW neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
KW cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
KW osteoporosis; inflammation; infection; psoriasis; wound healing.  
OS Synthetic.  
XX Key Location/Qualifiers  
XX Misc-difference 5 /note= "D-form residue"  
DE19933173-A1.  
18-JAN-2001.  
15-JUL-1999; 99DE-1033173.  
15-JUL-1999; 99DE-1033173.  
(MERE ) MERCK PATENT GMBH.  
Jonczyk A, Diefenbach B, Goodman S;  
WPI; 2001-192448/20.  
New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
useful e.g. for treating thrombosis, coronary heart disease, tumors,  
osteoporosis, inflammation or infections -  
Example 1; Page 11; 20pp; German.  
This invention describes novel cyclic peptides (I), containing 8 amino  
acid residues and optionally further alpha,omega-amino-carboxylic acid  
residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
Lys; R<sub>1</sub> = one or more omega-amino-carboxylic acid residues, having a  
length of 50-2500 mum; or is absent; the amino acid residues are  
optionally derivatized and include D- as well as L-forms (in the case of  
optically active aminoacids). The products of the invention have  
antiinflammatory, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
antiinflammatory, antibacterial, antipsoriatic, vulnery, ophthalmological,  
cerebroprotective, antianigmal, antidiabetic, antirheumatic, ophthalmological,  
antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
neuroprotective. (I) are used for treating diseases involving expression  
and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
wound healing deficiency. Other disclosed disorders to be treated include  
apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
retinopathy, macular degeneration, myopia, ocular histoplasmosis or  
rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
acute renal failure, renal inflammation or multiple sclerosis. (I) may  
also be useful in analytical biology and molecular biology; e.g.  
fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
used to prepare affinity chromatography columns for purifying integrins.  
DNA encoding (I) may be used for treating the same disorders as (I)  
itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
receptor inhibiting activity.

Sequence 12 AA;  
Query Match 100.0%; Score 20; DB 22; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
      ||||  
Db 3 DLDA 6

```
RESULT 33
AAW72284
ID AAW72284 standard; peptide; 13 AA.
XX
XX
AC AAW72284;
XX
DT 16-DEC-1998 (first entry)
XX
DE Dermatophagoides Der p I protein peptide DPI-26.3.
XX
KW genus Dermatophagoides; major protein allergen; T cell epitope;
KW Der p I; Der p II; Der f I; Der f II; house dust mite allergy.
XX
OS Dermatophagoides sp.
XX
XX US5820862-A.
XX
XX 13-OCT-1998.
XX
PF 07-JUN-1995; 95US-0482142.
XX
PR 19-MAY-1995; 95US-0445307.
PR 14-APR-1994; 94US-0227772.
PR 07-JUN-1995; 95US-0482142.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
PI Chen X, Evans S, Franzen HM, Garman RD, Greenstein JL;
PI Kuo M, Rogers BL, Shaked Z;
XX
XX WPI; 1998-567590/48.
XX
XX Dermatophagoides allergen peptides - useful for treating house dust
XX mite allergy
XX
XX Disclosure; Column 145-146; 155pp; English.
XX
CC The present invention describes peptides for treating sensitivity to
CC house dust mite allergens from the genus Dermatophagoides. Peptides
CC within the scope of the invention comprise at least one T cell epitope,
CC or preferably at least two T cell epitopes of a protein allergen
CC selected from the allergens Der p I, Der p II, Der f I, or Der f II.
CC The invention also describes modified peptides having similar or
CC enhanced therapeutic properties as the corresponding, naturally
CC occurring allergen, but having reduced side effects. AAW71912 to
CC AAW72000, and AAW72257 to AAW72330 represent peptides from the present
CC invention.
XX
XX Sequence 13 AA;
XX
Query Match 100.0%; Score 20; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 5 DLDA 8

RESULT 34
AAW50486
ID AAY50486 standard; Peptide; 13 AA.
XX
XX AAY50486;
XX
XX 25-JAN-2000 (first entry)
XX
XX Dermatophagoides sp major protein allergen DP I-26.3.
XX
DE Allergen; house dust mite; detection; sensitivity; T cell epitope;
KW screening; allergic disorder; asthma; rhinitis; ectopic dermatitis;
KW Der f I; Der p I; Der p II; Der f II.
```

```
XX Dermatophagoides sp.
XX
XX US5968526-A.
XX
XX 19-OCT-1999.
XX
XX 07-JUN-1995; 95US-0478572.
XX
XX 19-MAY-1995; 95US-0445307.
XX 14-APR-1994; 94US-0227772.
XX 12-APR-1995; 95WO-US04481.
XX
PA (IMMU-) IMMULOGIC PHARM CORP.
XX
XX Garman RD, Greenstein JL, Rogers BL, Franzen HM, Shaked Z, Chen X;
XX Evans S, Kuo M;
XX
XX WPI; 1999-590385/50.
XX
XX Screening individuals for allergic reactions to T cell epitopes of
XX major allergens from house dust mites -
XX
XX Claim 5w; Column 145-146; 158pp; English.
XX
CC This invention describes a novel method (I) for detecting whether an
CC individual is sensitive to Dermatophagoides (house dust mites). The
CC method involves detecting sensitivity to house dust mites in patients,
CC comprising combining a blood sample from the individual with 1 or more
CC isolated T cell epitopes of the protein allergens I and II (DP I) and
CC (DP II) from Dermatophagoides (house dust mites). 32 T cell epitopes
CC with varying, defined amino acids sequences (given in the specification)
CC may be used in (I). The sample and allergens are combined under
CC conditions appropriate for the binding of blood components with the
CC polypeptides. The extent of binding is then indicative of the
CC sensitivity of the patient to house dust mites. (I) may be used to screen
CC individuals for sensitivity to Dermatophagoides (house dust mites). The
CC house dust mite is a major cause of a variety of allergic disorders such
CC as asthma, rhinitis and ectopic dermatitis. AAY50360-Y50542 and
CC AAY50546-Y50555 represent house dust mite allergen peptide fragments
CC derived from Der p I, Der f II, Der f I and Der f II.
XX
XX Sequence 13 AA;
XX
Query Match 100.0%; Score 20; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 5 DLDA 8

RESULT 35
AAV39913
ID AAY39913 standard; peptide; 13 AA.
XX
XX AAY39913;
XX
XX 08-DEC-1999 (first entry)
XX
XX Paxillin LD1 peptide.
XX
KW Inhibitor; stereochemically diverse compound production; gene expression;
KW compound library generation; peptidomimetic compound; drug; HIV;
KW cellular proliferation; viral replication; cellular signalling process;
KW catalyst; E6-protein; E6-E6-AP pathway.
XX
XX Synthetic.
XX
XX WO9948897-A2.
XX
XX 30-SEP-1999.
```

XX PF 22-MAR-1999; 99WO-US06233.  
XX PR 23-MAR-1998; 98US-0079035.  
XX PR 22-MAR-1999; 99US-0079035.  
XX PA (HARD ) HARVARD COLLEGE.  
XX XX  
XX PI Verdine GL, Chytil M, Didiuk MT, Malinky T;  
XX XX WPI; 1999-580411/49.  
XX XX  
XX PT Generating libraries of stereochemically diverse compounds, especially  
XX PT peptidomimetics for use as pharmaceuticals -  
XX XX  
XX XX Disclosure; Fig 29; 123pp; English.  
XX XX  
XX CC This sequence represents the paxillin LD1 peptide, and was used to test  
XX CC compounds generated by the method of the invention, that were thought to  
XX CC be inhibitors of the E6-EG-AP pathway. The method is for generating a  
XX CC library of compounds having stereochemical diversity involving selecting  
XX CC desired synthetic precursors having a defined stereochemical  
XX CC relationship, reacting the synthetic precursors to give a compound having  
XX CC a specific stereochemistry and repeating the steps of selecting and  
XX CC reacting until the desired library is obtained. The method is useful for  
XX CC generating a library of peptidomimetic compounds having stereochemical  
XX CC diversity. The compounds may be useful as drugs, e.g. for control of HIV  
XX CC production, cellular proliferation, viral replication, gene expression or  
XX CC any other cellular signalling process. The compounds may be useful as  
XX CC catalysts, either as a ligand for a transition metal capable of mimicking  
XX CC a biological environment or by acting with a transition metal catalyst to  
XX CC effect a desired enantioselective chemical reaction. The compounds may  
XX CC further be useful for generating biomaterials.  
XX XX  
XX SQ Sequence 13 AA;  
XX  
XX Query Match 100.0%; Score 20; DB 20; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 DLDA 4  
XX ||||  
XX Db 1 DLDA 4  
XX  
XX  
XX RESULT 36  
XX AAB4689  
XX ID AAB4689 standard; peptide; 13 AA.  
XX AC  
XX AAB4689;  
XX  
XX DT 09-MAY-2001 (first entry)  
XX  
XX DE Integrin alpha-Vbeta-6 cyclic peptide inhibitor #21.  
XX  
XX Cyclic peptide; antithrombotic; cardiant; antiarteriosclerotic;  
XX cytostatic; osteopathic; antiinflammatory; antibacterial; antipsoriatic;  
XX vulnary; cerebroprotective; antianginal; antidiabetic; nephrotropic;  
XX ophthalmological; antiarthritic; antirheumatic; antiulcer; vasotropic;  
XX neuroprotective; alpha\_vbeta\_6-integrin receptor; thrombosis; tumor;  
XX cardiac infarction; coronary heart disease; arteriosclerosis; fibrosis;  
XX osteoporosis; inflammation; infection; psoriasis; wound healing.  
XX OS Synthetic.  
XX  
XX XX Key Location/Qualifiers  
XX FT Misc-difference 5 /note= "D-form residue"  
XX FT  
XX  
XX PN DE19933173-A1.  
XX XX  
XX PD 18-JAN-2001.  
XX XX

PE 15-JUL-1999; 99DE-1033173.  
XX  
XX PR 15-JUL-1999; 99DE-1033173.  
XX  
XX PA (MERE ) MERCK PATENT GMBH.  
XX  
XX PI Joneczyk A, Diefenbach B, Goodman S;  
XX XX WPI; 2001-192448/20.  
XX  
XX PT New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
XX PT useful e.g. for treating thrombosis, coronary heart disease, tumors,  
XX PT osteoporosis, inflammation or infections -  
XX XX  
XX PS Example 1; Page 11; 20pp; German.  
XX  
XX CC This invention describes novel cyclic peptides (I), containing 8 amino  
XX CC acid residues and optionally further alpha.omega-aminocarboxylic acid  
XX CC residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
XX CC X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
XX CC X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
XX CC Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
XX CC Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
XX CC length of 50-2500 mum; or is absent; the amino acid residues are  
XX CC optionally derivatized and include D- as well as L-forms (in the case of  
XX CC optically active aminoacids). The products of the invention have  
XX CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
XX CC antiinflammatory, antibacterial, antipsoriatic, vulnary,  
XX CC cerebroprotective, antianginal, antidiabetic, ophthalmological,  
XX CC antiarthritic, antirheumatic, antiulcer, vasotropic, nephrotropic,  
XX CC neuroprotective. (I) are used for treating diseases involving expression  
XX CC and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
XX CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
XX CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
XX CC wound healing deficiency. Other disclosed disorders to be treated include  
XX CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
XX CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or  
XX CC rheobitic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
XX CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
XX CC acute renal failure, renal inflammation or multiple sclerosis. (I) may  
XX CC also be useful in analytical biology and molecular biology; e.g.  
XX CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
XX CC used to prepare affinity chromatography columns for purifying integrins.  
XX CC DNA encoding (I) may be used for treating the same disorders as (I)  
XX CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
XX CC receptor inhibiting activity.  
XX  
XX SQ Sequence 13 AA;  
XX  
XX Query Match 100.0%; Score 20; DB 22; Length 13;  
XX Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 DLDA 4  
XX ||||  
XX Db 3 DLDA 6  
XX  
XX  
XX RESULT 37  
XX AAU19089  
XX ID AAU19089 standard; Peptide; 13 AA.  
XX XX  
XX AC AAU19089;  
XX  
XX XX  
XX DT 04-DEC-2001 (first entry)  
XX  
XX DE T-cell epitope containing peptide DPI-26.3.  
XX  
XX KW House dust mite; allergenic peptide; Der p I; Der p II; Der f I;  
XX KW Der f II; antiallergenic; immunostimulant; house dust mite allergy;  
XX KW T-cell epitope.  
XX  
XX OS Dermatophagoides pteronyssinus.





PI Jonczyk A, Diefenbach B, Goodman S;  
XX WPI; 2001-192448/20.  
XX  
XX  
XX New cyclic peptides, are alpha(v)beta(6) integrin receptor inhibitors  
PT useful e.g. for treating thrombosis, coronary heart disease, tumors,  
PT osteoporosis, inflammation or infections -  
XX  
XX  
XX  
XX  
XX Example 1; Page 10; 20pp; German.  
XX  
XX This invention describes novel cyclic peptides (I), containing 8 amino  
CC acid residues and optionally further alpha,omega-aminocarboxylic acid  
CC residues. Cyclic peptides of formula Cyclo-(Arg-X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-  
CC X<sub>5</sub>-X<sub>6</sub>-R<sub>1</sub>) (I) and their salts and solvates. X<sub>1</sub> = Ser, Gly or Thr;  
CC X<sub>2</sub> = Leu, Ile, Nle, Val or Phe; X<sub>3</sub> = Asp, Glu, Lys or Phe; X<sub>4</sub> =  
CC Gly, Ala or Ser; X<sub>5</sub> = Leu, Ile, Nle, Val or Phe; X<sub>6</sub> = Arg, Har or  
CC Lys; R<sub>1</sub> = one or more omega-aminocarboxylic acid residues, having a  
CC length of 50-2500 mum; or is absent; the amino acid residues are  
CC optionally derivatized and include D- as well as L-forms (in the case of  
CC optically active aminoacids). The products of the invention have  
CC antithrombotic, cardiant, antiarteriosclerotic, cytostatic, osteopathic,  
CC antiinflammatory, antibacterial, antipsoriatic, vulnerary,  
CC cerebroprotective, antianginal, antidiabetic, ophthalmological,  
CC antiarthritic, antirheumatic, antitumor, vasotropic, nephrotropic,  
CC neuroprotective (I) are used for treating diseases involving expression  
CC and pathological function of alpha\_vbeta\_6-integrin receptors, especially  
CC thrombosis, cardiac infarction, coronary heart disease, arteriosclerosis,  
CC tumors, osteoporosis, fibrosis, inflammation, infection, psoriasis and  
CC wound healing deficiency. Other disclosed disorders to be treated include  
CC apoplexy, angina pectoris, ophthalmological diseases (e.g. diabetic  
CC retinopathy, macular degeneration, myopia, ocular histoplasmosis or  
CC rubecotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative  
CC colitis, Crohn's disease, atherosclerosis, restenosis after angioplasty,  
CC acute renal failure, renal inflammation or multiple sclerosis. (I) may  
CC also be useful in analytical biology and molecular biology; e.g.  
CC fluorescently labeled (I) may be used as diagnostic markers or (I) may be  
CC used to prepare affinity chromatography columns for purifying integrins.  
CC DNA encoding (I) may be used for treating the same disorders as (I)  
CC itself. (I) are well tolerated and have good alpha\_vbeta\_6-integrin  
XX receptor inhibiting activity.  
XX  
XX  
SQ Sequence 14 AA;  
Query Match 100.0%; Score 20; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
|  
|  
|  
|  
Db 3 DLDA 6  
|  
|  
|  
|  
RESULT 40  
AAAR73948  
ID AAR73948 standard; Peptide; 15 AA.  
XX  
XX  
AC AAR73948;  
XX  
XX 04-DEC-1995 (first entry)  
DT  
XX  
XX Fragment of T.sergenti 33 kDa protein.  
DE  
XX  
XX bovine small piroplasma protozoa; 33 kDa protein; vaccine;  
KW immunogen.  
XX  
XX Theileria sergenti.  
OS  
XX  
XX AU9470373-A.  
PN  
XX  
XX 09-MAR-1995.  
PD  
XX  
XX 22-AUG-1994; 94AU-0070373.  
PF  
XX

PR 30-AUG-1993; 93JP-0238864.  
XX  
XX (NORQ ) NAT INST ANIMAL HEALTH.  
PA (KAGA ) CHERO SERO THERAPEUTIC RES INST.  
XX  
XX Fujisaki K, Kamio T, Kashiwazaki M, Kawazu S, Miyahara T;  
PI Nonaka F, Sakai E, Taneno A, Yamada S;  
XX  
XX WPI; 1995-147719/20.  
DR  
XX  
XX New bovine small piroplasma protozoa peptide(s) - contg. the  
PT Lys-Glu-Lys sequence, used for preventing infection or detecting  
PT antibodies.  
XX  
XX Claim 2; Page 16; 20pp; English.  
XX  
XX This sequence represents a fragment of the principal 33 kDa protein of  
CC T.sergenti (see also R73947). T.sergenti is a bovine small piroplasma  
CC protozoa. This sequence contains the KEK sequence which is the smallest  
CC immunogenic unit of the 33 kDa protein. This protein can be used in a  
CC vaccine for prevention of bovine small piroplasma disease.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 100.0%; Score 20; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
|  
|  
|  
|  
Db 12 DLDA 15  
|  
|  
|  
|  
RESULT 41  
AAW04908  
ID AAW04908 standard; Protein; 15 AA.  
XX  
XX AAW04908;  
AC  
XX 22-DEC-1996 (first entry)  
DT  
XX  
XX N. meningitidis 608B peptide CS-853.  
DE  
XX  
XX Proteinase K resistant; Neisseria meningitidis; epitope; mapping;  
KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.  
XX  
XX Synthetic.  
OS  
XX WO9629412-A1.  
PN  
XX 26-SEP-1996.  
PD  
XX  
XX 15-MAR-1996; 96WO-CA00157.  
PF  
XX  
XX 04-AUG-1995; 95US-0001983.  
PR  
XX 17-MAR-1995; 95US-0406362.  
XX  
XX (IAFB-) IAF BIO VAC INC.  
PA  
XX  
XX Brodeur BR, Hamel J, Martin D, Rioux C;  
PI  
XX WPI; 1996-443187/44.  
DR  
XX  
XX Neisseria meningitidis antigen, highly conserved between different  
PT strains - useful for prodn. of antibodies for immunisation against,  
PT or diagnosis of, N. meningitidis infection  
XX  
XX Claim 24; Page 82; 117pp; English.  
XX  
XX Example 9 describes the epitope mapping of the 22 kD  
CC N. meningitidis protein. Identification was accomplished  
CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).  
XX

```
SQ Sequence 15 AA;
  Query Match      100.0%; Score 20; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 12 DLDA 15

RESULT 42
AAW04909
ID AAW04909 standard; Protein; 15 AA.
XX
AC AAW04909;
XX
DT 22-DEC-1996 (first entry)
XX
DE N. meningitidis 608B peptide CS-854.
XX
KW Proteinase K resistant; Neisseria meningitidis; epitope; mapping;
KW Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
XX
OS Synthetic.
XX
PN WO9629412-A1.
XX
PD 26-SEP-1996.
XX
PF 15-MAR-1996; 96WO-CA00157.
XX
PR 04-AUG-1995; 95US-0001983.
PR 17-MAR-1995; 95US-0406362.
XX
XX (IAFB-) IAF BIO VAC INC.
XX
PI Brodeur BR, Hamel J, Martin D, Rioux C;
XX
DR WPI; 1996-443187/44.
XX
PT Neisseria meningitidis antigen, highly conserved between different
PT strains - useful for prodn. of antibodies for immunisation against,
PT or diagnosis of, N. meningitidis infection
XX
PS Claim 24; Page 83; 117pp; English.
XX
CC Example 9 describes the epitope mapping of the 22 kD
CC N. meningitidis protein. Identification was accomplished
CC using 18 overlapping synthetic peptides (AAW04895 to AAW04912).
XX
SQ Sequence 15 AA;
  Query Match      100.0%; Score 20; DB 17; Length 15;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 2 DLDA 5

RESULT 43
AAG64814
ID AAG64814 standard; Peptide; 15 AA.
XX
AC AAG64814;
XX
DT 19-SEP-2001 (first entry)
XX
DE Cytokine-like peptide screening method related peptide #14.
XX
KW Cytokine-like peptide; peptide mimic; viral disease.

XX OS Unidentified.
XX PN WO200148478-A1.
XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-JP09278.
XX PR 27-DEC-1999; 99JP-0369990.
XX (TORA ) TORAY IND INC.
XX Sato A, Sone S;
XX WPI; 2001-418329/44.
XX
XX Cytokine-like peptides screened by binding activity with antibody
XX having activity of neutralising cytokine, capable of expressing
XX biological activity of cytokine, useful as low-molecular peptide mimics
XX for treating e.g. viral diseases -
XX Example 10; Fig 7; 33pp; Japanese.
XX
XX The present invention describes a method of screening a cytokine-like
XX peptide, comprising searching for a peptide, which is capable of
XX expressing the biological activity of the cytokine, by binding to an
XX antibody which has an activity of neutralising a cytokine, from amongst
XX peptides not having been confirmed as being with the biological activity
XX of the cytokine. The peptides identified using the method are applicable
XX as low-molecular peptide mimics of cytokine for treating e.g. viral
XX diseases.
XX
XX SQ Sequence 15 AA;
  Query Match      100.0%; Score 20; DB 22; Length 15;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    ||||
Db 11 DLDA 14

RESULT 44
ABB44423
ID ABB44423 standard; Peptide; 18 AA.
XX
AC ABB44423;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #11929 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
```

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
XX Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human fetal liver -  
XX  
XX Claim 27; SEQ ID NO 37058; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
XX measuring human gene expression in a sample derived from human foetal  
XX liver. The single exon nucleic acid probes may be used for predicting,  
XX measuring and displaying gene expression in samples derived from human  
XX fetal liver. The present sequence is a peptide encoded by a single exon  
XX nucleic acid probe of the invention.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 18 AA;  
XX  
XX Query Match 100.0%; Score 20; DB 22; Length 18;  
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 1 DLDA 4  
XX ||||  
XX Db 3 DLDA 6  
XX  
XX RESULT 45  
XX ABB27270  
XX ID ABB27270 standard; Protein; 18 AA.  
XX  
XX AC ABB27270;  
XX  
XX DT 23-JAN-2002 (first entry)  
XX  
XX DE Protein #9269 encoded by probe for measuring heart cell gene expression.  
XX  
XX KW Human; gene expression; heart; microarray; vascular system;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200157274-A2.  
XX  
XX PD 09-AUG-2001.  
XX  
XX PF 30-JAN-2001; 2001WO-US00666.  
XX  
XX PR 04-FEB-2000; 2000US-0180312.  
XX PR 26-MAY-2000; 2000US-0207456.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234687.  
XX PR 27-SEP-2000; 2000US-0236359.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX DR WPI; 2001-488899/53.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts -  
XX  
XX PS Claim 15; SEQ ID NO 29040; 530pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX SQ Sequence 18 AA;  
XX  
XX Query Match 100.0%; Score 20; DB 22; Length 18;  
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Qy 1 DLDA 4  
XX ||||  
XX Db 3 DLDA 6  
XX  
XX Search completed: February 6, 2003, 11:19:36  
XX Job time : 28.8333 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 : Search time 9.33333 Seconds  
(without alignments)  
12.610 Million cell updates/sec

Title: PAT943-2  
Perfect score: 20  
Sequence: 1 dlida 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 634

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	6	2	US-08-763-302-2
2	20	100.0	6	4	US-09-177-595-2
3	20	100.0	8	2	US-08-568-310D-3
4	20	100.0	8	4	US-08-817-811-4
5	20	100.0	8	4	US-08-817-811-5
6	20	100.0	8	4	US-09-270-455-3
7	20	100.0	12	4	US-08-817-811-9
8	20	100.0	12	4	US-08-817-811-23
9	20	100.0	12	4	US-08-817-811-24
10	20	100.0	12	4	US-08-817-811-25
11	20	100.0	12	4	US-08-817-811-29
12	20	100.0	13	2	US-08-482-142-135
13	20	100.0	13	2	US-08-478-572-135
14	20	100.0	13	4	US-08-484-296-135
15	20	100.0	15	4	US-08-913-362-22
16	20	100.0	15	4	US-08-913-362-23
17	20	100.0	18	4	US-08-477-928A-24
18	20	100.0	20	1	US-08-171-299B-16
19	20	100.0	20	4	US-08-817-811-1
20	20	100.0	20	4	US-08-817-811-37
21	20	100.0	24	4	US-09-314-242-9
22	20	100.0	26	1	US-08-057-161-2
23	20	100.0	26	2	US-08-482-142-21
24	20	100.0	26	2	US-08-482-142-22
25	20	100.0	26	2	US-08-482-142-37
26	20	100.0	26	2	US-08-482-142-134
27	20	100.0	26	2	US-08-482-142-168

Sequence 21, Appl  
Sequence 22, Appl  
Sequence 37, Appl  
Sequence 134, App  
Sequence 168, App  
Sequence 4, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 37, Appl  
Sequence 134, App  
Sequence 168, App  
Sequence 4, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 37, Appl  
Sequence 134, App  
Sequence 168, App  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 30, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-08-763-302-2  
; Sequence 2, Application US/08763302  
; Patent No. 5932692  
; GENERAL INFORMATION:  
; APPLICANT: FASSINA, GIORGIO  
; APPLICANT: VERDOLIVA, ANTONIO  
; APPLICANT: RUVO, MENOTTI  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/763.302  
; FILING DATE: 10-DEC-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IT MI95A002582  
; FILING DATE: 11-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B.J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 2149-101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-763-302-2

Query Match 100.0%; Score 20; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

Db 2 DLDA 5  
||||

## RESULT 2

US-09-177-595-2  
; Sequence 2, Application US/09177595  
; Patent No. 622011  
; GENERAL INFORMATION:  
; APPLICANT: FASSINA, GIORGIO  
; APPLICANT: VERDOLIVA, ANTONIO  
; APPLICANT: ROVO, MEMOTTI  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22201  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/177,595  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/763,302  
; FILING DATE: 10-DEC-1996  
; APPLICATION NUMBER: IT MI95A002582  
; FILING DATE: 11-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SADOFF, B. J.  
; REGISTRATION NUMBER: 36,663  
; REFERENCE/DOCKET NUMBER: 2149-101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-816-4000  
; TELEFAX: 703-816-4100  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-177-595-2

Query Match 100.0%; Score 20; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||

Db 2 DLDA 5

## RESULT 3

US-08-568-310D-3  
; Sequence 3, Application US/08568310D  
; Patent No. 5976832  
; GENERAL INFORMATION:  
; APPLICANT: HITOMI, JIRO  
; APPLICANT: YAMAGUCHI, KEN  
; APPLICANT: YAMAMURA, TOKUJIRO  
; APPLICANT: KIMURA, TATSUJI  
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WYATT, GERBER, MELLER, & O'ROURKE

; STREET: 99 PARK AVENUE  
; STREET: 6th FLOOR  
; CITY: NEW YORK CITY  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb  
; MEDIUM TYPE: STORAGE  
; COMPUTER: IBM-PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS 6.2  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/568,310D  
; FILING DATE: DECEMBER 6, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)  
; FILING DATE: 3/6/95 and 3/6/95, respectively  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KLEIN, MILTON  
; REGISTRATION NUMBER: 27101  
; REFERENCE/DOCKET NUMBER: 3316  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)953-3350  
; TELEFAX: (212)953-3352  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; PUBLICATION INFORMATION:  
; RELEVANT RESIDUES IN SEQ ID NO: 3:  
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 8  
US-08-568-310D-3

Query Match 100.0%; Score 20; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||

Db 4 DLDA 7

## RESULT 4

US-08-817-811-4  
; Sequence 4, Application US/08817811  
; Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,811  
; FILING DATE: 14-APR-1997

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-817-811-4

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 4 DLDA 7

RESULT 5  
US-08-817-811-5  
Sequence 5, Application US/08817811  
Patent No. 6174528  
GENERAL INFORMATION:  
APPLICANT: Cooper, Juan A.  
APPLICANT: Relif, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-817-811-5

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 2 DLDA 5

RESULT 6  
US-09-270-455-3  
Sequence 3, Application US/09270455  
Patent No. 6313267  
GENERAL INFORMATION:  
APPLICANT: HITOMI, JIRO  
APPLICANT: YAMAGUCHI, KEN  
APPLICANT: YAMAMURA, TOKUJIRO  
APPLICANT: KIMURA, TATSUJI  
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE  
STREET: 99 PARK AVENUE  
CITY: NEW YORK CITY  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb  
MEDIUM TYPE: STORAGE  
COMPUTER: IBM-PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS 6.2  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/270,455  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/568,310  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KLEIN, MILTON  
REGISTRATION NUMBER: 27101  
REFERENCE/DOCKET NUMBER: 3316  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)953-3350  
TELEFAX: (212)953-3352  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 8  
US-09-270-455-3

Query Match 100.0%; Score 20; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 4 DLDA 7

RESULT 7  
US-08-817-811-9  
Sequence 9, Application US/08817811  
Patent No. 6174528  
GENERAL INFORMATION:

APPLICANT: Cooper, Juan A.  
APPLICANT: Relf, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
TITLE OF INVENTION: COMPRISING SAME  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-817-811-9  
Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 4 DLDA 7  
RESULT 8  
US-08-817-811-23  
Sequence 23, Application US/08817811  
Patent No. 6174528  
GENERAL INFORMATION:  
APPLICANT: Cooper, Juan A.  
APPLICANT: Relf, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
TITLE OF INVENTION: COMPRISING SAME  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-817-811-23  
Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 4 DLDA 7  
RESULT 9  
US-08-817-811-24  
Sequence 24, Application US/08817811  
Patent No. 6174528  
GENERAL INFORMATION:  
APPLICANT: Cooper, Juan A.  
APPLICANT: Relf, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
TITLE OF INVENTION: COMPRISING SAME  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids



;  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-817-811-24

Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 3 DLDA 6

RESULT 10  
US-08-817-811-25  
; Sequence 25, Application US/08817811  
; Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-817-811-25  
Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 2 DLDA 5

RESULT 11  
US-08-817-811-29  
; Sequence 29, Application US/08817811  
; Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

US-08-817-811-25  
Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 2 DLDA 5

RESULT 12  
US-08-817-811-135  
; Sequence 135, Application US/08482142  
; Patent No. 5820862  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA

GENERAL INFORMATION:  
APPLICANT: Cooper, Juan A.  
APPLICANT: Relf, Wendy A.  
APPLICANT: Good, Michael F.  
APPLICANT: Saul, Allan J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,811  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION NUMBER: WO 96/11944  
FILING DATE: 25-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: FBRC:005  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-817-811-29  
Query Match 100.0%; Score 20; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 1 DLDA 4

RESULT 12  
US-08-482-142-135  
; Sequence 135, Application US/08482142  
; Patent No. 5820862  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA

ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-482-142-135

Query Match 100.0%; Score 20; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 5 DLDA 8

## RESULT 13

US-08-478-572-135  
Sequence 135, Application US/08478572  
Patent No. 5968526  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,572  
FILING DATE: 07-June-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-478-572-135

Query Match 100.0%; Score 20; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 5 DLDA 8

## RESULT 14

US-08-484-296-135  
Sequence 135, Application US/08484296  
Patent No. 6268491  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FRAGMENT TYPE: internal  
US-08-484-296-135

Query Match 100.0%; Score 20; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 5 DLDA 8

RESULT 15

US-08-913-362-22  
; Sequence 22, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913.362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Neisseria meningitidis  
; STRAIN: 608B  
US-08-913-362-22

Query Match 100.0%; Score 20; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 12 DLDA 15

RESULT 16

US-08-913-362-23  
; Sequence 23, Application US/08913362  
; Patent No. 6287574  
; GENERAL INFORMATION:  
; APPLICANT: Brodeur, Bernard R  
; APPLICANT: Martin, Denis  
; APPLICANT: Hamel, Josee  
; APPLICANT: Rioux, Clement  
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/913,362  
; FILING DATE: 13-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,362  
; FILING DATE: 17-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,983  
; FILING DATE: 04-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 047998/0128  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Neisseria meningitidis  
; STRAIN: 608B  
US-08-913-362-23

Query Match 100.0%; Score 20; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 2 DLDA 5

RESULT 17

US-08-477-928A-24  
; Sequence 24, Application US/08477928A  
; Patent No. 6207389  
; GENERAL INFORMATION:  
; APPLICANT: Dosch, Hans M.  
; TITLE OF INVENTION: METHODS FOR CONTROLLING T  
; TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKER & BOTTS  
; STREET: 1299 Pennsylvania Avenue

; CITY: Washington D.C.  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,928A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remenick, James  
; REGISTRATION NUMBER: 36902  
; REFERENCE/DOCKET NUMBER: 19060-0105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 639 7700  
; TELEFAX: (202) 639 7890  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-477-928A-24

Query Match 100.0%; Score 20; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 8 DLDA 11

RESULT 18  
US-08-171-299B-16  
; Sequence 16, Application US/08171299B  
; Patent No. 5599665  
; GENERAL INFORMATION:  
; APPLICANT: Barbieri, Joseph T.  
; APPLICANT: Frank, Dara W.  
; TITLE OF INVENTION: EXOENZYME S' PROTEIN PREPARATION AND CLONED EXOENZYME S  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: QUARLES & BRADY  
; STREET: 411 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: U.S.A.  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/171,299B  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baker, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 650053.90871  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5709  
; TELEFAX: (414) 271-3552  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-171-299B-16

Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 2 DLDA 5

RESULT 19  
US-08-817-811-1  
; Sequence 1, Application US/08817811  
; Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; TITLE OF INVENTION: COMPRISING SAME  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,811  
; FILING DATE: 14-APR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 96/11944  
; FILING DATE: 25-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: FBRC:005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-817-811-1

Query Match 100.0%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 4 DLDA 7

RESULT 20  
US-08-817-811-37  
; Sequence 37, Application US/08817811

Patent No. 6174528  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Juan A.  
; APPLICANT: Relf, Wendy A.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Saul, Allan J.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
; TITLE OF INVENTION: COMPRISING SAME  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,811  
; FILING DATE: 14-APR-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: WO 96/11944  
; FILING DATE: 25-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: FBRC:005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-817-811-37

Query Match 100.0%; Score 20; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 14 DLDA 17

RESULT 21  
US-09-314-242-9  
; Sequence 9, Application US/09314242A  
; Patent No. 6248575  
; GENERAL INFORMATION:  
; APPLICANT: Elizabeth J. Golightly  
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides  
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity  
; FILE REFERENCE: 5556.200-US  
; CURRENT APPLICATION NUMBER: US/09/314,242A  
; CURRENT FILING DATE: 1999-05-18  
; EARLIER APPLICATION NUMBER: 09/080,428  
; EARLIER FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Trichoderma harzianum  
; FEATURE:  
; OTHER INFORMATION: Xaa = The amino acid residue was not determinable.

US-09-314-242-9

Query Match 100.0%; Score 20; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 8 DLDA 11

RESULT 22  
US-08-057-161-2  
; Sequence 2, Application US/08057161  
; Patent No. 5371189  
; GENERAL INFORMATION:  
; APPLICANT: Helderman, J. H.  
; TITLE OF INVENTION: MONOCYTE-DERIVED INSULIN RECEPTOR  
; TITLE OF INVENTION: REGULATORY FACTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
; STREET: 133 Carnegie Way, N.W., Suite 400  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/057,161  
; FILING DATE: 19930430  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 2200.011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; TISSUE TYPE: Monocyte  
; CELL TYPE: P388D1 (ATCC Accession No. 5371189 TIB 63)  
US-08-057-161-2

Query Match 100.0%; Score 20; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 16 DLDA 19

RESULT 23  
US-08-482-142-21  
; Sequence 21, Application US/08482142  
; Patent No. 5820862  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia

APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-482-142-21

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||  
Db 15 DLDA 18

RESULT 24  
US-08-482-142-22  
Sequence 22, Application US/08482142,  
Patent No. 5820862  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM

STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-482-142-22

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||  
Db 3 DLDA 6

RESULT 25  
US-08-482-142-37  
Sequence 37, Application US/08482142  
Patent No. 5820862  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-482-142-37

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 6 DLDA 9

RESULT 26  
US-08-482-142-134  
Sequence 134, Application US/08482142  
Patent No. 5820862  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-482-142-134

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 6 DLDA 9

RESULT 27  
US-08-482-142-168  
Sequence 168, Application US/08482142  
Patent No. 5820862  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 168:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-482-142-168

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 6 DLDA 9

## RESULT 28

US-08-478-572-21  
; Sequence 21, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,572  
; FILING DATE: 07-June-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017.6US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
; US-08-478-572-21

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 15 DLDA 18

## RESULT 29

US-08-478-572-22  
; Sequence 22, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; US-08-478-572-22

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 15 DLDA 18

APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,572  
FILING DATE: 07-June-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-478-572-22

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 3 DLDA 6

## RESULT 30

US-08-478-572-37  
; Sequence 37, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; US-08-478-572-37

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. le+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 3 DLDA 6



; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,572  
; FILING DATE: 07-June-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017.605  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
; US-08-478-572-37

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 6 DLDA 9

RESULT 31  
US-08-478-572-134  
; Sequence 134, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,572  
; FILING DATE: 07-June-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976

; REFERENCE/DOCKET NUMBER: 017.605  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-08-478-572-134

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 6 DLDA 9

RESULT 32  
US-08-478-572-168  
; Sequence 168, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,572  
; FILING DATE: 07-June-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017.605  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 168:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-08-478-572-168

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 6 DLDA 9

RESULT 33  
US-08-987-289-4  
; Sequence 4, Application US/08987289  
; Patent No. 5994098  
; GENERAL INFORMATION:  
; APPLICANT: HU, ERDING  
; APPLICANT: ZHU, YUAN  
; TITLE OF INVENTION: A Human 7-TM Receptor Similar  
; TITLE OF INVENTION: to Murine Frizzled-6 gene  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980  
; CITY: VALLEY FORGE  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19482  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/987,289  
; FILING DATE: 09-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,725  
; FILING DATE: 02-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PRESTIA, PAUL F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GH-70060  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-987-289-4

Query Match 100.0%; Score 20; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 19 DLDA 22

RESULT 34  
US-08-484-296-21  
; Sequence 21, Application US/08484296  
; Patent No. 6268491  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce

; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,296  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE: 07 June 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017,605  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal  
US-08-484-296-21

Query Match 100.0%; Score 20; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 15 DLDA 18

RESULT 35  
US-08-484-296-22  
; Sequence 22, Application US/08484296  
; Patent No. 6268491  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA

ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.60S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-484-296-22

Query Match 100.0%; Score 20; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 3 DLDA 6

RESULT 36  
US-08-484-296-37  
Sequence 37, Application US/08484296  
Patent No. 6268491  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE: 07 June 1995

ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.60S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-484-296-37

Query Match 100.0%; Score 20; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 6 DLDA 9

RESULT 37  
US-08-484-296-134  
Sequence 134, Application US/08484296  
Patent No. 6268491  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.60S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal  
US-08-484-296-134

Query Match 100.0%; Score 20; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 6 DLDA 9

## RESULT 38

US-08-484-296-168  
; Sequence 168, Application US/08484296  
; Patent No. 6268491

## GENERAL INFORMATION:

; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,296  
; FILING DATE:

## CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE: 07 June 1995  
; ATTORNEY/AGENT INFORMATION:

; NAME: CRAIG, ANNE I.

; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017.6US  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6040

; INFORMATION FOR SEQ ID NO: 168:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-484-296-168

Query Match 100.0%; Score 20; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 6 DLDA 9

## RESULT 39

PCT-US95-04481-12  
; Sequence 12, Application PC/TUS9504481  
; GENERAL INFORMATION:

## APPLICANT:

; TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dus-  
; NUMBER OF SEQUENCES: 54  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04481  
; FILING DATE:

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/227,772  
; FILING DATE: April 14, 1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: Vanstone, Darlene A.

; REGISTRATION NUMBER: 35,279

; REFERENCE/DOCKET NUMBER: 017.5 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6040

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

PCT-US95-04481-12

Query Match 100.0%; Score 20; DB 5; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 15 DLDA 18

## RESULT 40

PCT-US95-04481-13

; Sequence 13, Application PC/TUS9504481  
; GENERAL INFORMATION:

## APPLICANT:

; TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dust  
; NUMBER OF SEQUENCES: 54  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04481  
; FILING DATE:

## CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/227,772  
; FILING DATE: April 14, 1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: Vanstone, Darlene A.

; REGISTRATION NUMBER: 35,279

; REFERENCE/DOCKET NUMBER: 017.5 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6040

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

;  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
PCT-US95-04481-13

Query Match 100.0%; Score 20; DB 5; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 3 DLDA 6

RESULT 41  
PCT-US95-04481-30  
; Sequence 30, Application PC/TUS9504481  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Pharmaceutical Peptide Formulations For Treatment of Dust Mit  
; NUMBER OF SEQUENCES: 54  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04481  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/227,772  
; FILING DATE: April 14, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vanstone, Darlene A.  
; REGISTRATION NUMBER: 35,279  
; REFERENCE/DOCKET NUMBER: 017.5 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
PCT-US95-04481-30

Query Match 100.0%; Score 20; DB 5; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 6 DLDA 9

RESULT 42  
US-08-141-324-12  
; Sequence 12, Application US/08141324  
; Patent No. 5475097  
; GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; CLASSIFICATION: Protease

; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/141,324  
; FILING DATE: 21-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 44-93  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 303-499-8080  
; TELEFAX: 303-499-8089  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-141-324-12

Query Match 100.0%; Score 20; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 7 DLDA 10

RESULT 43  
US-08-541-902-12  
; Sequence 12, Application US/08541902  
; Patent No. 5707620  
; GENERAL INFORMATION:  
; APPLICANT: Travis, James  
; APPLICANT: Potempa, Jan S.  
; APPLICANT: Barr, Philip J.  
; APPLICANT: Pavloff, Nadine  
; APPLICANT: Pike, Robert N.  
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee and Winner, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/541,902  
; FILING DATE:  
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/141,324  
;; FILING DATE: 21-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ferber, Donna M.  
;; REGISTRATION NUMBER: 33,878  
;; REFERENCE/DOCKET NUMBER: 44-93  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 303-499-8080  
;; TELEFAX: 303-499-8089  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
US-08-541-902-12

Query Match 100.0%; Score 20; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 7 DLDA 10

;; RESULT 44  
;; US-08-817-811-13  
;; Sequence 13, Application US/08817811  
;; Patent No. 6174528  
;; GENERAL INFORMATION:  
;; APPLICANT: Cooper, Juan A.  
;; APPLICANT: Relf, Wendy A.  
;; APPLICANT: Good, Michael F.  
;; APPLICANT: Saul, Allan J.  
;; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
;; NUMBER OF SEQUENCES: 97  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: P.O. Box 4433  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: USA  
;; ZIP: 77210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 14-APR-1997  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO 96/11944  
;; FILING DATE: 25-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Highlander, Steven L.  
;; REGISTRATION NUMBER: 37,642  
;; REFERENCE/DOCKET NUMBER: FBRC:005  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 512/418-3000  
;; TELEFAX: 512/474-7577  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:

;; TOPOLOGY: linear  
US-08-817-811-13

Query Match 100.0%; Score 20; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 12 DLDA 15

;; RESULT 45  
;; US-08-817-811-14  
;; Sequence 14, Application US/08817811  
;; Patent No. 6174528  
;; GENERAL INFORMATION:  
;; APPLICANT: Cooper, Juan A.  
;; APPLICANT: Relf, Wendy A.  
;; APPLICANT: Good, Michael F.  
;; APPLICANT: Saul, Allan J.  
;; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES  
;; NUMBER OF SEQUENCES: 97  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Arnold, White & Durkee  
;; STREET: P.O. Box 4433  
;; CITY: Houston  
;; STATE: Texas  
;; COUNTRY: USA  
;; ZIP: 77210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/817,811  
;; FILING DATE: 14-APR-1997  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO 96/11944  
;; FILING DATE: 25-APR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Highlander, Steven L.  
;; REGISTRATION NUMBER: 37,642  
;; REFERENCE/DOCKET NUMBER: FBRC:005  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 512/418-3000  
;; TELEFAX: 512/474-7577  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 28 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
US-08-817-811-14

Query Match 100.0%; Score 20; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 11 DLDA 14

Search completed: February 6, 2003, 11:24:04  
Job time : 10.3333 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 11:22:09 ; Search time 5.83333 Seconds  
(without alignments)  
15.202 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 419

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US03\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	20	100.0	18	10	US-09-864-761-42568
2	20	100.0	18	10	US-09-299-473A-2
3	20	100.0	20	9	US-10-044-034-22
4	20	100.0	26	10	US-09-740-516-4
5	20	100.0	33	10	US-09-746-919-38
6	20	100.0	40	12	US-10-025-167-45
7	20	100.0	50	9	US-09-932-172A-2
8	20	100.0	50	9	US-09-955-581-2
9	20	100.0	50	9	US-10-039-119A-2
10	20	100.0	50	10	US-09-864-761-39240
11	20	100.0	50	10	US-09-299-473A-1
12	20	100.0	52	10	US-09-864-761-39301
13	20	100.0	58	10	US-09-864-761-43108
14	20	100.0	62	9	US-09-738-626-5087
15	20	100.0	63	9	US-09-738-626-4594
16	20	100.0	63	10	US-09-867-550-466
17	20	100.0	65	10	US-09-864-761-42283
18	20	100.0	65	10	US-09-864-761-43617
19	20	100.0	74	10	US-09-815-242-13358

20	20	100.0	77	10	US-09-815-242-13674
21	20	100.0	81	10	US-09-867-550-320
22	20	100.0	89	9	US-09-738-626-5626
23	20	100.0	89	10	US-09-819-930-2
24	20	100.0	89	10	US-09-819-930-4
25	20	100.0	89	10	US-09-755-187-2
26	20	100.0	90	10	US-09-826-589-3
27	20	100.0	90	10	US-09-826-589-4
28	20	100.0	90	10	US-09-872-185B-11
29	20	100.0	90	10	US-09-872-185B-12
30	20	100.0	94	10	US-09-864-761-48068
31	20	100.0	95	9	US-09-981-353-98
32	20	100.0	95	10	US-09-746-919-24
33	20	100.0	95	10	US-09-956-425-18
34	20	100.0	95	10	US-09-956-425-21
35	20	100.0	95	10	US-09-956-425-22
36	20	100.0	95	10	US-09-956-425-23
37	20	100.0	95	10	US-09-919-172-102
38	20	100.0	97	10	US-09-746-919-28
39	20	100.0	98	10	US-09-915-582-51
40	20	100.0	98	10	US-09-915-582-67
41	20	100.0	99	10	US-09-746-919-22
42	20	100.0	101	9	US-09-738-626-3769
43	20	100.0	102	10	US-09-746-919-26
44	20	100.0	109	12	US-10-062-254-76
45	20	100.0	117	9	US-09-906-209-6

ALIGNMENTS

RESULT 1

- US-09-864-761-42568
- ; Sequence 42568, Application US/09864761
- ; Patent No. US20020048763A1
- ; GENERAL INFORMATION:
- ; APPLICANT: Penn, Sharon G.
- ; APPLICANT: Rank, David R.
- ; APPLICANT: Hanzel, David K.
- ; APPLICANT: Chen, Wensheng
- ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY
- ; FILE REFERENCE: Aecomica-X-1
- ; CURRENT APPLICATION NUMBER: US/09/864,761
- ; CURRENT FILING DATE: 2001-05-23
- ; PRIOR APPLICATION NUMBER: US 60/180,312
- ; PRIOR FILING DATE: 2000-02-04
- ; PRIOR APPLICATION NUMBER: US 60/207,456
- ; PRIOR FILING DATE: 2000-05-26
- ; PRIOR APPLICATION NUMBER: US 09/632,366
- ; PRIOR FILING DATE: 2000-08-03
- ; PRIOR APPLICATION NUMBER: GB 24263.6
- ; PRIOR FILING DATE: 2000-10-04
- ; PRIOR APPLICATION NUMBER: US 60/236,359
- ; PRIOR FILING DATE: 2000-09-27
- ; PRIOR APPLICATION NUMBER: PCT/US01/00666
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00667
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00664
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00669
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00665
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00668
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00663
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00662
- ; PRIOR FILING DATE: 2001-01-30
- ; PRIOR APPLICATION NUMBER: PCT/US01/00661
- ; PRIOR FILING DATE: 2001-01-30

Sequence 13674, A  
Sequence 320, App  
Sequence 5626, Ap  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 4, Appli  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 48068, A  
Sequence 98, Appl  
Sequence 24, Appl  
Sequence 18, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 23, Appl  
Sequence 102, App  
Sequence 28, Appl  
Sequence 51, Appl  
Sequence 67, Appl  
Sequence 3769, Ap  
Sequence 26, Appl  
Sequence 76, Appl  
Sequence 6, Appli

; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 42568  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL133246.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9  
; OTHER INFORMATION: EST\_HUMAN HIT: A0117241.1, EVALUATE 2.50e-01  
US-09-864-761-42568

Query Match 100.0%; Score 20; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 3 DLDA 6

## RESULT 2

US-09-299-473A-2  
; Sequence 2, Application US/09299473A  
; Patent No. US20020099008A1  
; GENERAL INFORMATION:  
; APPLICANT: Twardzik, Daniel R  
; APPLICANT: Felker, Thomas S  
; APPLICANT: Stefan, Paskell L  
; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR  
; TITLE OF INVENTION: STIMULATING STEM CELL PROLIFERATION AND MIGRATION  
; FILE REFERENCE: STEMI100  
; CURRENT APPLICATION NUMBER: US/09/299,473A  
; CURRENT FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-299-473A-2

Query Match 100.0%; Score 20; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 15 DLDA 18

## RESULT 3

US-10-044-034-22  
; Sequence 22, Application US/10044034  
; Patent No. US20020169264A1  
; GENERAL INFORMATION:  
; APPLICANT: JACKSON, DAVID C.  
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.  
; APPLICANT: BROWN, LORENA E.

; APPLICANT: EDE, NICHOLAS J.  
; APPLICANT: BRANDT, EVELYN R.  
; APPLICANT: GOOD, MICHAEL F.  
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES  
; FILE REFERENCE: FBRC:006  
; CURRENT APPLICATION NUMBER: US/10/044,034  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: P05071  
; PRIOR FILING DATE: 1997-02-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptides  
US-10-044-034-22

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 4 DLDA 7

## RESULT 4

US-09-740-516-4  
; Sequence 4, Application US/09740516  
; Patent No. US20010011124A1  
; GENERAL INFORMATION:  
; APPLICANT: HU, ERDING  
; APPLICANT: ZHU, YUAN  
; TITLE OF INVENTION: A HUMAN 7-TM RECEPTOR SIMILAR TO MURINE  
; TITLE OF INVENTION: FRIZZLED-6 GENE  
; FILE REFERENCE: GH-70060-DIC1  
; CURRENT APPLICATION NUMBER: US/09/740,516  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 08/987,289  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: 09/304,485  
; PRIOR FILING DATE: 1999-05-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-740-516-4

Query Match 100.0%; Score 20; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 19 DLDA 22

## RESULT 5

US-09-746-919-38  
; Sequence 38, Application US/09746919  
; Patent No. US20020013452A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:



ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US 09/746,919  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/045,467  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/438,753  
FILING DATE: 10-MAY-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,891  
FILING DATE: 19-OCT-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,741  
FILING DATE: 09-MAR-1992  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/318,050  
FILING DATE: 02-MAR-1989  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/969,890  
FILING DATE: 30-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J.  
REGISTRATION NUMBER: 28,006  
REFERENCE/DOCKET NUMBER: 5600-0001.36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Amino acid sequence of fragment  
INDIVIDUAL ISOLATE: 90-122 of SEQ ID NO:33  
US-09-746-919-38

Query Match 100.0%; Score 20; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 6 DLDA 9

RESULT 6  
US-10-025-167-45  
Sequence 45, Application US/10025167  
Patent No. US20020127693A1  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA A.  
COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
HAYDEN, MARK  
KLASS, MICHAEL R.  
ROBERTS-RAPP, LISA  
RUSSELL, JOHN C.

TITLE OF INVENTION: REAGENTS AND METHODS FOR THE  
USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
TRACT  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/025,167  
FILING DATE: 19-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/049,698  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/828,856  
FILING DATE: 31-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6068.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. US20020127693A1e  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-025-167-45

Query Match 100.0%; Score 20; DB 12; Length 40;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 15 DLDA 18

RESULT 7  
US-09-932-172A-2  
Sequence 2, Application US/09932172A  
Patent No. US20020169119A1  
GENERAL INFORMATION:  
APPLICANT: STEM CELL PHARMACEUTICALS, INC.  
APPLICANT: TWARDZIK, Daniel R.  
APPLICANT: PERNET, Andre  
APPLICANT: FELKER, Thomas S.  
APPLICANT: PASKELL, Stefan  
TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF  
FILE REFERENCE: STEM1110-3  
CURRENT APPLICATION NUMBER: US/09/932.172A  
CURRENT FILING DATE: 2001-08-17  
PRIORITY APPLICATION NUMBER: US 09/641,587  
PRIORITY FILING DATE: 2000-08-17  
PRIORITY APPLICATION NUMBER: US 09/492,935  
PRIORITY FILING DATE: 2000-01-27  
PRIORITY APPLICATION NUMBER: US 09/378,567  
PRIORITY FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-932-172A-2

Query Match 100.0%; Score 20; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 47 DLDA 50

## RESULT 8

US-09-955-581-2  
; Sequence 2, Application US/09955581  
; Patent No. US20020169131A1  
; GENERAL INFORMATION:  
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.  
; APPLICANT: TWARDZIK, Daniel  
; APPLICANT: PASKELL, Stefan  
; APPLICANT: FELKER, Thomas  
; TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USE  
; FILE REFERENCE: STEM1100-3  
; CURRENT APPLICATION NUMBER: US/09/955,581  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 09/559,248  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 09/299,473  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: US 09/459,813  
; PRIOR FILING DATE: 1999-12-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-955-581-2

Query Match 100.0%; Score 20; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 47 DLDA 50

## RESULT 9

US-10-039-119A-2  
; Sequence 2, Application US/10039119A  
; Publication No. US20020193301A1  
; GENERAL INFORMATION:  
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.  
; APPLICANT: TWARDZIK, Daniel R.  
; APPLICANT: PERNET, Andre  
; APPLICANT: FELKER, Thomas S.  
; APPLICANT: PASKELL, Stefan  
; TITLE OF INVENTION: TGF-alpha POLYPEPTIDES, FUNCTIONAL FRAGMENTS AND METHODS OF USE  
; FILE REFERENCE: STEM110-4  
; CURRENT APPLICATION NUMBER: US/10/039,119A  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US 09/641,587  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: US 09/492,935  
; PRIOR FILING DATE: 2000-01-17  
; PRIOR APPLICATION NUMBER: US 09/378,567  
; PRIOR FILING DATE: 1999-08-19

; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-039-119A-2

Query Match 100.0%; Score 20; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 47 DLDA 50

## RESULT 10

US-09-864-761-39240  
; Sequence 39240, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annotax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 39240  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Homo sapiens

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;
; FEATURE:
; OTHER INFORMATION: MAP TO AC005701.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: P39057, EVALUE 2.00e-04
US-09-864-761-39240

Query Match          100.0%; Score 20; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 32 DLDA 35

RESULT 11
US-09-299-473A-1
; Sequence 1, Application US/09299473A
; Patent No. US20020099008A1
; GENERAL INFORMATION:
; APPLICANT: Twardzik, Daniel R
; APPLICANT: Felker, Thomas S
; APPLICANT: Stefan, Paskell L
; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR
; FILE REFERENCE: STEM1100
; CURRENT APPLICATION NUMBER: US/09/299,473A
; CURRENT FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-299-473A-1

Query Match          100.0%; Score 20; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 47 DLDA 50

RESULT 12
US-09-864-761-39301
; Sequence 39301, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
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;
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39301
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005155.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: SWISSPROT HIT: P29972, EVALUE 2.00e-24
; OTHER INFORMATION: EST_HUMAN HIT: BF477059.1, EVALUE 3.00e-23
US-09-864-761-39301

Query Match          100.0%; Score 20; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 38 DLDA 41

RESULT 13
US-09-864-761-43108
; Sequence 43108, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
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; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263,6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 43108  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL035416.7  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1  
; OTHER INFORMATION: SWISSPROT HIT: P32892, EVALUATE 2.00e+00  
US-09-864-761-43108

Query Match 100.0%; Score 20; DB 10; Length 58;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 33 DLDA 36  
|||||

RESULT 14  
US-09-738-626-5087  
; Sequence 5087, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIALI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENO, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125

; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 5087  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5087

Query Match 100.0%; Score 20; DB 9; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 8 DLDA 11  
|||||

RESULT 15  
US-09-738-626-4594  
; Sequence 4594, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIALI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENO, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 4594  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4594

Query Match 100.0%; Score 20; DB 9; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 27 DLDA 30  
|||||

RESULT 16  
US-09-867-550-466  
; Sequence 466, Application US/09867550  
; Patent No. US20020082206A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.

; APPLICANT: Mehraban, Fuad.  
; APPLICANT: Conley, Pamela  
; APPLICANT: Law, Debbie  
; APPLICANT: Topper, James  
; TITLE OF INVENTION: No. US20020082206Ae1 Polynucleotides from Atherogenic Cells and  
; TITLE OF INVENTION: Thereby  
; FILE REFERENCE: 21402-013 (Cura-313)  
; CURRENT APPLICATION NUMBER: US/09/867,550  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: USSN 60/208,427  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 2125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 466  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-867-550-466

Query Match 100.0%; Score 20; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
Db 2 DLDA 5

RESULT 17  
US-09-864-761-42283  
; Sequence 42283, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 42283  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC018720.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8  
; OTHER INFORMATION: EST HUMAN HIT: BE720191.1, EVALUATE 3.00e-31  
; OTHER INFORMATION: SWISSPROT HIT: P53972, EVALUATE 6.00e-02  
US-09-864-761-42283

Query Match 100.0%; Score 20; DB 10; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
Db 6 DLDA 9

RESULT 18  
US-09-864-761-43617  
; Sequence 43617, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aeomica-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43617
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002036.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
; OTHER INFORMATION: EST_HUMAN HIT: AA434168.1, EVALUE 2.00e-32
; OTHER INFORMATION: SWISSPROT HIT: P57080, EVALUE 2.00e-13
US-09-864-761-43617
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Query Match          100.0%; Score 20; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 DLDA 4
    ||||
Db 45 DLDA 48
```

## RESULT 19

```
US-09-815-242-13358
; Sequence 13358, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
```

```
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 74
```

```
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13358
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```
Query Match          100.0%; Score 20; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DLDA 4
    ||||
Db 30 DLDA 33
```

## RESULT 20

```
US-09-815-242-13674
; Sequence 13674, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

```
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
```

```
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13674
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
```

```
US-09-815-242-13674
```

```
Query Match          100.0%; Score 20; DB 10; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DLDA 4
    ||||
Db 33 DLDA 36
```

## RESULT 21

```
US-09-867-550-320
; Sequence 320, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Fuad,
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells
```

; TITLE OF INVENTION: Thereby  
; FILE REFERENCE: 21402-013 (Cura-313)  
; CURRENT APPLICATION NUMBER: US/09/867,550  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: USSN 60/208,427  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 2125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 320  
; LENGTH: 81  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-867-550-320

Query Match 100.0%; Score 20; DB 10; Length 81;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 1 DLDA 4

RESULT 22  
US-09-738-626-5626  
; Sequence 5626, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 5626  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5626

Query Match 100.0%; Score 20; DB 9; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 85 DLDA 88

RESULT 23  
US-09-819-930-2  
; Sequence 2, Application US/09819930  
; Patent No. US20020090700A1  
; GENERAL INFORMATION:  
; APPLICANT: FARWICK, MIKE  
; APPLICANT: MOCKEL, BETTINA  
; APPLICANT: PFEFFERLE, WALTER

; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING THE PTSH GENE  
; FILE REFERENCE: MAS/21123/278412  
; CURRENT APPLICATION NUMBER: US/09/819,930  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 09/755,187  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: DE 100 01 101.2  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-819-930-2

Query Match 100.0%; Score 20; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 85 DLDA 88

RESULT 24  
US-09-819-930-4  
; Sequence 4, Application US/09819930  
; Patent No. US20020090700A1  
; GENERAL INFORMATION:  
; APPLICANT: FARWICK, MIKE  
; APPLICANT: MOCKEL, BETTINA  
; APPLICANT: PFEFFERLE, WALTER  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING THE PTSH GENE  
; FILE REFERENCE: MAS/21123/278412  
; CURRENT APPLICATION NUMBER: US/09/819,930  
; CURRENT FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 09/755,187  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: DE 100 01 101.2  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-819-930-4

Query Match 100.0%; Score 20; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 85 DLDA 88

RESULT 25  
US-09-755-187-2  
; Sequence 2, Application US/09755187  
; Patent No. US20020094554A1  
; GENERAL INFORMATION:  
; APPLICANT: Farwick, Mike  
; APPLICANT: Mockel, Bettina  
; APPLICANT: Pfefferle, Walter  
; TITLE OF INVENTION: New Nucleotide Sequences Encoding the PTSH Gene  
; FILE REFERENCE: 21123/275573  
; CURRENT APPLICATION NUMBER: US/09/755,187  
; CURRENT FILING DATE: 2001-01-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2

; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-755-187-2

Query Match 100.0%; Score 20; DB 10; Length 89;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 85 DLDA 88

RESULT 26  
US-09-826-589-3  
; Sequence 3, Application US/09826589  
; Patent No. US20020106726A1

; GENERAL INFORMATION:  
; APPLICANT: Stern, David  
; APPLICANT: Schmidt, Ann Marie  
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE  
; FILE REFERENCE: 0575/55873-B-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/826,589  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-826-589-3

Query Match 100.0%; Score 20; DB 10; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 59 DLDA 62

RESULT 27  
US-09-826-589-4  
; Sequence 4, Application US/09826589  
; Patent No. US20020106726A1

; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Stern, David  
; TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE  
; FILE REFERENCE: 0575/55873-B-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/826,589  
; CURRENT FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-826-589-4

Query Match 100.0%; Score 20; DB 10; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 59 DLDA 62

RESULT 28  
US-09-872-185B-11  
; Sequence 11, Application US/09872185B

; Patent No. US20020122799A1  
; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Herold, Kevan  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Lamster, Ira  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
; FILE REFERENCE: 0575/64080  
; CURRENT APPLICATION NUMBER: US/09/872,185B  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-872-185B-11

Query Match 100.0%; Score 20; DB 10; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 59 DLDA 62

RESULT 29  
US-09-872-185B-12  
; Sequence 12, Application US/09872185B  
; Patent No. US20020122799A1

; GENERAL INFORMATION:  
; APPLICANT: Stern, David M.  
; APPLICANT: Herold, Kevan  
; APPLICANT: Yan, Shi Du  
; APPLICANT: Schmidt, Ann Marie  
; APPLICANT: Lamster, Ira  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION  
; FILE REFERENCE: 0575/64080  
; CURRENT APPLICATION NUMBER: US/09/872,185B  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Bovine  
US-09-872-185B-12

Query Match 100.0%; Score 20; DB 10; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 59 DLDA 62

RESULT 30  
US-09-864-761-48068  
; Sequence 48068, Application US/09864761  
; Patent No. US20020048763A1

; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23



;; PRIOR APPLICATION NUMBER: US 60/180,312  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: US 09/632,366  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 48068  
;; LENGTH: 94  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AC009594.2  
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3  
;; OTHER INFORMATION: EST HUMAN HIT: A1962273.1, EVALUE 5.00e-17  
;; OTHER INFORMATION: SWISSPROT HIT: Q95155, EVALUE 1.00e-23  
;; NAME/KEY: unsure  
;; LOCATION: 8  
US-09-864-761-48068

Query Match 100.0%; Score 20; DB 10; Length 94;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 48 DLDA 51

RESULT 31  
US-09-981-353-98  
; Sequence 98, Application US/09981353  
; Patent No. US20020160382A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
; FILE REFERENCE: PA-0038 US  
; CURRENT APPLICATION NUMBER: US/09/981,353  
; CURRENT FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PERL Program

;; SEQ ID NO 98  
;; LENGTH: 95  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; OTHER INFORMATION: Incyte ID No. US20020160382A1 1422432CD1  
US-09-981-353-98

Query Match 100.0%; Score 20; DB 9; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 60 DLDA 63

RESULT 32  
US-09-746-919-24  
; Sequence 24, Application US/09746919  
; Patent No. US20020013452A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/746,919  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/045,467  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/438,753  
; FILING DATE: 10-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 28,006  
; REFERENCE/DOCKET NUMBER: 5600-0001.36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 95 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; INDIVIDUAL ISOLATE: Of SEQ ID NO:23 (HuIFNtau7).  
US-09-746-919-24

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 56 DLDA 59

## RESULT 33

US-09-956-425-18  
; Sequence 18, Application US/09956425;  
; Patent No. US20020045192A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriwacki, Richard  
; APPLICANT: Bothner, Brian  
; APPLICANT: Lewis, William  
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
; FILE REFERENCE: 1340/1/035  
; CURRENT APPLICATION NUMBER: US/09/956,425  
; CURRENT FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-956-425-18

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

## RESULT 34

US-09-956-425-21  
; Sequence 21, Application US/09956425;  
; Patent No. US20020045192A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriwacki, Richard  
; APPLICANT: Bothner, Brian  
; APPLICANT: Lewis, William  
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
; FILE REFERENCE: 1340/1/035  
; CURRENT APPLICATION NUMBER: US/09/956,425  
; CURRENT FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: horse  
US-09-956-425-21

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 35  
US-09-956-425-22  
; Sequence 22, Application US/09956425  
; Patent No. US20020045192A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriwacki, Richard  
; APPLICANT: Bothner, Brian  
; APPLICANT: Lewis, William  
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
; FILE REFERENCE: 1340/1/035  
; CURRENT APPLICATION NUMBER: US/09/956,425  
; CURRENT FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: dog  
US-09-956-425-22

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

## RESULT 36

US-09-956-425-23  
; Sequence 23, Application US/09956425  
; Patent No. US20020045192A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriwacki, Richard  
; APPLICANT: Bothner, Brian  
; APPLICANT: Lewis, William  
; TITLE OF INVENTION: Arf and Hdm2 Interaction Domains and Method of Use Thereof  
; FILE REFERENCE: 1340/1/035  
; CURRENT APPLICATION NUMBER: US/09/956,425  
; CURRENT FILING DATE: 2001-09-19  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: chicken  
US-09-956-425-23

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

## RESULT 37

US-09-919-172-102  
; Sequence 102, Application US/09919172  
; Patent No. US20020119463A1  
; GENERAL INFORMATION:  
; APPLICANT: Faris, Mary  
; APPLICANT: Turner, Christopher M.  
; TITLE OF INVENTION: PROSTATE CANCER MARKERS  
; FILE REFERENCE: PA-0036 US  
; CURRENT APPLICATION NUMBER: US/09/919,172  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/222,469  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PERL Program  
; SEQ ID NO 102  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1422432CD1  
US-09-919-172-102

Query Match 100.0%; Score 20; DB 10; Length 95;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 60 DLDA 63

RESULT 38  
US-09-746-919-28  
; Sequence 28, Application US/09746919  
; Patent No. US20020013452A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Howard M.  
; APPLICANT: Pontzer, Carol H.  
; TITLE OF INVENTION: Interferon Tau Compositions and  
; TITLE OF INVENTION: Methods of Use  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Ave., Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/746,919  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/045,467  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/438,753  
; FILING DATE: 10-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,891  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,741  
; FILING DATE: 09-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/318,050  
; FILING DATE: 02-MAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/969,890  
; FILING DATE: 30-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dehlinger, Peter J.  
; REGISTRATION NUMBER: 28,006  
; REFERENCE/DOCKET NUMBER: 5600-0001.36  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-324-0880  
; TELEFAX: 650-324-0960  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 97 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
; OF SEQ ID NO:27 (HuIFNtau5).  
US-09-746-919-28

Query Match 100.0%; Score 20; DB 10; Length 97;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 56 DLDA 59

RESULT 39  
US-09-915-582-51  
; Sequence 51, Application US/09915582  
; Patent No. US20020120103A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 17 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/09/915,582  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-915-582-51

Query Match 100.0%; Score 20; DB 10; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 73 DLDA 76

RESULT 40  
US-09-915-582-67  
; Sequence 67, Application US/09915582  
; Patent No. US20020120103A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 17 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/09/915,582  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 67

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; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-582-67

Query Match      100.0%; Score 20; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 73 DLDA 76

RESULT 41
US-09-746-919-22
; Sequence 22, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746.919
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,467
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,753
; FILING DATE: 10-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,891
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,741
; FILING DATE: 09-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,050
; FILING DATE: 02-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,890
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 5600-0001.36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: predicted amino acid coding sequence

; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HuIFNtau6).
US-09-746-919-22

Query Match      100.0%; Score 20; DB 10; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 56 DLDA 59

RESULT 42
US-09-738-626-3769
; Sequence 3769, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3769
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3769

Query Match      100.0%; Score 20; DB 9; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

RESULT 43
US-09-746-919-26
; Sequence 26, Application US/09746919
; Patent No. US20020013452A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Interferon Tau Compositions and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/746,919  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,467  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/438,753  
FILING DATE: 10-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,891  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/847,741  
FILING DATE: 09-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/318,050  
FILING DATE: 02-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/969,890  
FILING DATE: 30-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dehlinger, Peter J.  
REGISTRATION NUMBER: 28,006  
REFERENCE/DOCKET NUMBER: 5600-0001.36  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0960  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: predicted amino acid coding sequence  
INDIVIDUAL ISOLATE: of SEQ ID NO:25 (Huifntaud).  
US-09-746-919-26

Query Match 100.0%; Score 20; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 56 DLDA 59

RESULT 44  
US-10-062-254-76  
; Sequence 76, Application US/10062254  
; Patent No. US20020138882A1  
; GENERAL INFORMATION:  
; APPLICANT: Cahoon, Edgar B  
; APPLICANT: Cahoon, Rebecca E  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Fang, Yiwen  
; APPLICANT: Hantke, Sabine S.  
; APPLICANT: Lee, Jian-Ming  
; APPLICANT: Li, Zhongsen  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Morgante, Michele  
; APPLICANT: Niu, Xiping  
; APPLICANT: Odell, Joan  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Zheng, Peizhong  
; APPLICANT: Zhu, Qun  
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metabolism

FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/062,254  
CURRENT FILING DATE: 2002-02-01  
PRIOR APPLICATION NUMBER: 09/630,346  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: 60/146511  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: 60/156006  
PRIOR FILING DATE: 1999-09-23  
PRIOR APPLICATION NUMBER: 60/156899  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: 60/157287  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: 60/169767  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/171054  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: 60/172958  
PRIOR FILING DATE: 1999-12-21  
PRIOR APPLICATION NUMBER: 60/171515  
PRIOR FILING DATE: 1999-12-22  
PRIOR APPLICATION NUMBER: 60/173535  
PRIOR FILING DATE: 1999-12-29  
NUMBER OF SEQ ID NOS: 375  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 76  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Triticum aestivum  
US-10-062-254-76

Query Match 100.0%; Score 20; DB 12; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
||||  
Db 93 DLDA 96

RESULT 45  
US-09-906-209-6  
; Sequence 6, Application US/09906209  
; Patent No. US20020165385A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Butler, Karla  
; APPLICANT: Carlson, Tom  
; APPLICANT: Ilag, Lawrence L.  
; TITLE OF INVENTION: Plastidic Phosphoglucumutase Genes  
; FILE REFERENCE: BB1451 NA  
; CURRENT APPLICATION NUMBER: US/09/906,209  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,712  
; PRIOR FILING DATE: JULY 17, 2000  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 6  
; LENGTH: 117  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (108)  
; OTHER INFORMATION: n = A, C, G, or T  
US-09-906-209-6

Query Match 100.0%; Score 20; DB 9; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
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Thu Feb 6 12:30:07 2003

Db 83 DLDA 86

Search completed: February 6, 2003, 11:39:43  
Job time : 6.83333 secs

pat943-2.rapb

Page 16

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:59 ; Search time 133.167 Seconds  
(without alignments)  
19.366 Million cell updates/sec

Title: PAT943-2  
Perfect score: 20  
Sequence: 1 dlda 4

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues  
Total number of hits satisfying chosen parameters: 10241

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Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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- 10: /cgn2\_6/ptodata/1/paa/US15\_COMB.pap.\*
- 11: /cgn2\_6/ptodata/1/paa/US16\_COMB.pap.\*
- 12: /cgn2\_6/ptodata/1/paa/US17\_COMB.pap.\*
- 13: /cgn2\_6/ptodata/1/paa/US18\_COMB.pap.\*
- 14: /cgn2\_6/ptodata/1/paa/US19\_COMB.pap.\*
- 15: /cgn2\_6/ptodata/1/paa/US20\_COMB.pap.\*
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- 19: /cgn2\_6/ptodata/1/paa/US24\_COMB.pap.\*
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- 21: /cgn2\_6/ptodata/1/paa/US26\_COMB.pap.\*
- 22: /cgn2\_6/ptodata/1/paa/US27\_COMB.pap.\*
- 23: /cgn2\_6/ptodata/1/paa/US28\_COMB.pap.\*
- 24: /cgn2\_6/ptodata/1/paa/US29\_COMB.pap.\*
- 25: /cgn2\_6/ptodata/1/paa/US30\_COMB.pap.\*
- 26: /cgn2\_6/ptodata/1/paa/US31\_COMB.pap.\*
- 27: /cgn2\_6/ptodata/1/paa/US32\_COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	7	25	US-10-130-157-226
2	20	100.0	8	9	US-08-568-3100-3
3	20	100.0	9	12	US-08-864-983A-10
4	20	100.0	10	22	US-09-800-187-54
5	20	100.0	11	18	US-09-461-774-20
6	20	100.0	13	6	US-08-227-772-135

7	20	100.0	13	8	US-08-445-307A-135
8	20	100.0	13	16	US-09-373-597-3
9	20	100.0	14	1	PCT-US98-20991-4
10	20	100.0	15	20	US-09-884-883-22
11	20	100.0	15	20	US-09-884-883-23
12	20	100.0	17	8	US-09-437-413-2
13	20	100.0	18	1	PCT-US01-00663-38679
14	20	100.0	18	6	US-08-237-363-24
15	20	100.0	18	16	US-09-299-473A-2
16	20	100.0	18	22	US-09-864-761-42568
17	20	100.0	18	25	US-10-182-993-37608
18	20	100.0	18	25	US-10-182-995-29040
19	20	100.0	18	25	US-10-182-997-26863
20	20	100.0	18	26	US-10-203-134-38471
21	20	100.0	18	26	US-10-203-136-38459
22	20	100.0	18	26	US-10-203-137-38679
23	20	100.0	18	26	US-10-203-139-37058
24	20	100.0	19	19	US-09-512-563-43
25	20	100.0	19	19	US-09-512-563A-43
26	20	100.0	19	19	US-09-512-563C-43
27	20	100.0	20	3	US-07-698-925A-1
28	20	100.0	20	13	US-08-944-147-22
29	20	100.0	20	13	US-08-944-147-22
30	20	100.0	20	24	US-10-044-034-22
31	20	100.0	21	3	US-07-946-304-2
32	20	100.0	22	3	US-07-969-314A-10
33	20	100.0	22	14	US-09-080-428-9
34	20	100.0	25	21	US-09-724-059-530377
35	20	100.0	25	21	US-09-724-059-530378
36	20	100.0	25	21	US-09-724-059-530379
37	20	100.0	25	21	US-09-724-059-53338
38	20	100.0	25	21	US-09-724-059-53338
39	20	100.0	25	21	US-09-724-059-538495
40	20	100.0	25	21	US-09-724-059-538496
41	20	100.0	25	21	US-09-724-059-559241
42	20	100.0	25	21	US-09-724-059-559242
43	20	100.0	25	21	US-09-724-059-559243
44	20	100.0	25	21	US-09-724-059-559244
45	20	100.0	25	21	US-09-724-059-559245
			25	21	US-09-724-059-559246

ALIGNMENTS

RESULT 1  
US-10-130-157-226  
; Sequence 226, Application US/10130157  
; GENERAL INFORMATION:  
; APPLICANT: GENENTECH GmbH  
; TITLE OF INVENTION: The Genome of the HIV-1 Inter-Subtype (C/B') and Use Thereof  
; FILE REFERENCE: WAG-001 PCT  
; CURRENT APPLICATION NUMBER: US/10/130.157  
; CURRENT FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: DE 19955089.1  
; PRIOR FILING DATE: 1999-11-16  
; NUMBER OF SEQ ID NOS: 379  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 226  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-130-157-226

Query Match 100.0%; Score 20; DB 25; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 2 DLDA 5

RESULT 2

US-08-568-310C-3  
; Sequence 3, Application US/08568310C.  
; GENERAL INFORMATION:  
; APPLICANT: HITOMI, JIRO  
; APPLICANT: YAMAGUCHI, KEN  
; APPLICANT: YAMAMURA, TOKUJIRO  
; APPLICANT: KIMURA, TATSUJI  
; TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MELLER AND ASSOCIATES  
; STREET: 50 EAST 42nd STREET  
; STREET: 19th FLOOR  
; CITY: NEW YORK CITY  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 KB  
; MEDIUM TYPE: STORAGE  
; COMPUTER: IBM-PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS 6.2  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/568-310C  
; FILING DATE: DECEMBER 6, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)  
; FILING DATE: 3/6/95 and 3/6/95, respectively  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Klein, Milton  
; REGISTRATION NUMBER: 27101  
; REFERENCE/DOCKET NUMBER: 3316  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)953-3350  
; TELEFAX: (212)953-3352  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; PUBLICATION INFORMATION:  
; RELEVANT RESIDUES IN SEQ ID NO: 3:  
; RELEVANT RESIDUES IN SEQ ID NO: FROM 1 TO 8  
US-08-568-310C-3  
Query Match 100.0%; Score 20; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 4 DLDA 7  
RESULT 3  
US-08-864-983A-10  
; Sequence 10, Application US/08864983A  
; GENERAL INFORMATION:  
; APPLICANT: Kawauchi, Yasushi  
; APPLICANT: Takasaki, Jun  
; APPLICANT: Yasunaga, Tomoe  
; APPLICANT: Masuho, Yasuhiko  
; TITLE OF INVENTION: NOVEL MONOCLONAL ANTIBODY HAVING  
; TITLE OF INVENTION: INHIBITORY ACTIVITY AGAINST TYPE II PHOSPHOLIPASE A2 AND  
; TITLE OF INVENTION: PROTEIN COMPRISING A PART THEREOF  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 Pennsylvania Avenue, N.W.  
; CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/864,983A  
FILING DATE: 29-MAY-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/02714  
FILING DATE: 27-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP HEI 6-340006  
FILING DATE: 29-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Nakamura, Dean H.  
REGISTRATION NUMBER: 33,981  
REFERENCE/DOCKET NUMBER: O-45511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-7860  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL LINE: 1.4  
US-08-864-983A-10  
Query Match 100.0%; Score 20; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 4.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 1 DLDA 4  
RESULT 4  
US-09-800-187-54  
; Sequence 54, Application US/09800187  
; GENERAL INFORMATION:  
; APPLICANT: GROZINGER, CHRISTINA M.  
; APPLICANT: HASSIG, CHRISTIAN A.  
; APPLICANT: SCHREIBER, STUART L.  
; TITLE OF INVENTION: CLASS II HUMAN HISTONE DEACETYLASES, AND USES RELATED  
; TITLE OF INVENTION: THERETO  
; FILE REFERENCE: HUV-037.01  
; CURRENT APPLICATION NUMBER: US/09/800,187  
; CURRENT FILING DATE: 2001-03-05  
; PRIOR APPLICATION NUMBER: 60/186,802  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-187-54  
Query Match 100.0%; Score 20; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 1 DLDA 4



Db 3 DLDA 6

## RESULT 5

US-09-461-774-20  
; Sequence 20, Application US/09461774  
; GENERAL INFORMATION:  
; APPLICANT: CHAN, Lily  
; APPLICANT: CHUNG, Maxey Ching Ming  
; APPLICANT: LIM, Renee Lay Hong  
; TITLE OF INVENTION: Bacterial-derived molecules and therapeutic and  
; FILE OF INVENTION: diagnostic uses therefor  
; FILE REFERENCE: 1781-0180P  
; CURRENT APPLICATION NUMBER: US/09/461,774  
; CURRENT FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-461-774-20

Query Match 100.0%; Score 20; DB 18; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 7 DLDA 10

## RESULT 6

US-08-227-772-135  
; Sequence 135, Application US/08227772  
; GENERAL INFORMATION:  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET SUITE 510  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/227,772  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,396  
FILING DATE: 08-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: MANDRAGOURAS, AMY E.  
REGISTRATION NUMBER: P36,207  
REFERENCE/DOCKET NUMBER: IMI-012/IPC-017C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-227-772-135

Query Match 100.0%; Score 20; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 5 DLDA 8

## RESULT 7

US-08-445-307A-135  
; Sequence 135, Application US/08445307A  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307A  
FILING DATE: 07 June 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.60S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-445-307A-135

Query Match 100.0%; Score 20; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 5 DLDA 8

## RESULT 8

US-09-273-597-3  
; Sequence 3, Application US/09273597  
; GENERAL INFORMATION:

```
; APPLICANT: Verdine, Greg L.
; APPLICANT: Chytil, Milan
; APPLICANT: Malinky, Tiffany
; APPLICANT: Diduk, Mary T.
; TITLE OF INVENTION: SYNTHESIS OF COMPOUNDS AND LIBRARIES OF
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 00246-258001
; CURRENT APPLICATION NUMBER: US/09/273,597
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079,035
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-273-597-3

Query Match          100.0%; Score 20; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
   ||||
Db 1 DLDA 4

RESULT 9
PCT-US98-20991-4
; Sequence 4; Application PC/TUS9820991
; GENERAL INFORMATION:
; APPLICANT: New England Medical Center Hospitals, Inc.
; TITLE OF INVENTION: STRUCTURE-BASED RATIONAL DESIGN OF COMPOUNDS TO INHIBIT
; TITLE OF INVENTION: PAPILLOMA VIRUS INFECTION
; FILE REFERENCE: 00398/135W01
; CURRENT APPLICATION NUMBER: PCT/US98/20991
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: US 60/961,295
; EARLIER FILING DATE: 1997-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US98-20991-4

Query Match          100.0%; Score 20; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 3 DLDA 6

RESULT 10
US-09-684-883-22
; Sequence 22; Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
```

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; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,362
; FILING DATE: 13-NOV-1997
; APPLICATION NUMBER: US 08/406,362
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: US 60/001,983
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 047998/0128
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Neisseria meningitidis
; STRAIN: 608B
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-684-883-22

Query Match          100.0%; Score 20; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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Db 12 DLDA 15

RESULT 11
US-09-684-883-23
; Sequence 23; Application US/09684883
; GENERAL INFORMATION:
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; APPLICANT: Hamel, Josee
; APPLICANT: Rioux, Clement
; TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
; TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/684,883
; FILING DATE: 06-Oct-2000
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US/08/913.362  
FILING DATE: 13-NOV-1997  
APPLICATION NUMBER: US 08/406.362  
FILING DATE: 17-MAR-1995  
APPLICATION NUMBER: US 60/001.983  
FILING DATE: 04-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 047998/0128  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Neisseria meningitidis  
STRAIN: 608B  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-684-883-23

Query Match 100.0%; Score 20; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 2 DLDA 5

RESULT 12  
US-08-437-413-2  
Sequence 2, Application US/08437413  
GENERAL INFORMATION:  
APPLICANT: PERRYMAN, M. BENJAMIN  
APPLICANT: WU, ALAN  
APPLICANT: FRIEDMAN, DAVID  
APPLICANT: HAMBURG, ROBERT  
APPLICANT: ROBERTS, ROBERT  
TITLE OF INVENTION: METHOD OF DETERMINING SERUM OR  
TITLE OF INVENTION: PLASMA MITOCHONDRIAL CREATINE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/437,413  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/007,994  
FILING DATE: JANUARY 11, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA S. KITCHELL  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: BAYM:008/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200

TELEFAX: 512-474-7577  
TELEX: NOT APPLICABLE  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-437-413-2

Query Match 100.0%; Score 20; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 8 DLDA 11

RESULT 13  
PCT-US01-00663-38679  
Sequence 38679, Application PC/TUS0100663  
GENERAL INFORMATION:  
APPLICANT: Molecular Dynamics, Inc.  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FILE REFERENCE: PB 0004 WO 7  
CURRENT APPLICATION NUMBER: PCT/US01/00663  
CURRENT FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 04 February 2000 (04..02.00)  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 26 May 2000 (26.05.00)  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 03 August 2000 (03.08.00)  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 03 October 2000 (03.10.00)  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 27 September 2000 (27.09.00)  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 21 September 2000 (21.09.00)  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 30 June 2000 (30.06.00)  
NUMBER OF SEQ ID NOS: 38837  
SOFTWARE: Molecular Dynamics Sequence Listing Engine  
SEQ ID NO 38679  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL13246.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
OTHER INFORMATION: EST\_HUMAN HIT: AUL17241.1, EVALUATE 2.50e-01  
PCT-US01-00663-38679

Query Match 100.0%; Score 20; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
DB 3 DLDA 6

RESULT 14  
US-08-237-363-24  
Sequence 24, Application US/08237363  
GENERAL INFORMATION:  
APPLICANT: DOSCH, HANS MICHAEL

;; TITLE OF INVENTION: METHODS FOR CONTROLLING T LYMPHOCYTE  
;; TITLE OF INVENTION: MEDIATED IMMUNE RESPONSES  
;; NUMBER OF SEQUENCES: 29  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BAKER & BOTTS  
;; STREET: The Warner, 1299 Pennsylvania Avenue, N.W.  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20004-2400  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/237/363  
;; FILING DATE: 03-MAY-1994  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Remenick, James  
;; REGISTRATION NUMBER: 36902  
;; REFERENCE/DOCKET NUMBER: 19060-0104  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-639-7700  
;; TELEFAX: 202-639-7890  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-237-363-24

Query Match 100.0%; Score 20; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||  
DB 8 DLDA 11

RESULT 15  
US-09-299-473A-2  
;; Sequence 2, Application US/09299473A  
;; GENERAL INFORMATION:  
;; APPLICANT: Twardzik, Daniel R  
;; APPLICANT: Felker, Thomas S  
;; APPLICANT: Stefan, Paskell L  
;; TITLE OF INVENTION: LOOP PEPTIDE AND TGF ALPHA FOR  
;; TITLE OF INVENTION: STIMULATING STEM CELL PROLIFERATION AND MIGRATION  
;; FILE REFERENCE: STEMI100  
;; CURRENT APPLICATION NUMBER: US/09/299,473A  
;; CURRENT FILING DATE: 1999-04-26  
;; NUMBER OF SEQ ID NOS: 4  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-299-473A-2

Query Match 100.0%; Score 20; DB 16; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||  
DB 15 DLDA 18

RESULT 16  
US-09-864-761-42568  
;; Sequence 42568, Application US/09864761  
;; GENERAL INFORMATION:  
;; APPLICANT: Penn, Sharron G.  
;; APPLICANT: Rank, David R.  
;; APPLICANT: Hanzel, David K.  
;; APPLICANT: Chen, Wensheng  
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
;; FILE REFERENCE: Aeomica-X-1  
;; CURRENT APPLICATION NUMBER: US/09/864,761  
;; CURRENT FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/180,312  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: US 09/632,366  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 42568  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AL13246.1  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5  
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9  
;; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUE 2.50e-01  
US-09-864-761-42568

Query Match 100.0%; Score 20; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||

Db 3 DLDA 6

## RESULT 17

US-10-182-993-37608  
; Sequence 37608, Application US/10182993  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: PB 0004 WO 2  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/10/182,993  
; PRIOR FILING DATE: 04 February 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 37608  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO ALL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN HUMAN BRAIN  
; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUATE 2.50e-01  
US-10-182-993-37608

Query Match 100.0%; Score 20; DB 25; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

## RESULT 18

US-10-182-995-29040  
; Sequence 29040, Application US/10182995  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: PB 0004 WO 1  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/10/182,993  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 29119  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 29040  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO ALL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6  
; FEATURE:  
; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUATE 2.50e-01  
US-10-182-995-29040

Query Match 100.0%; Score 20; DB 25; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 3 DLDA 6

## RESULT 19

US-10-182-997-26863  
; Sequence 26863, Application US/10182997  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: PB 0004 WO 10  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/10/182,997  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 26941  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 26863  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO ALL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.5  
; FEATURE:  
; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUATE 2.50e-01  
US-10-182-997-26863

Query Match 100.0%; Score 20; DB 25; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 3 DLDA 6

## RESULT 20

US-10-203-134-38471  
; Sequence 38471, Application US/10203134  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: PB 0004 WO 6  
; CURRENT APPLICATION NUMBER: US/10/203,134  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 38628  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 38471  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9  
; FILE REFERENCE: EST\_HUMAN HIT: AUI17241.1, EVALUE 2.50e-01  
US-10-203-134-38471

Query Match 100.0%; Score 20; DB 26; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 3 DLDA 6

## RESULT 21

US-10-203-136-38459  
; Sequence 38459, Application US/10203136  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: PB 0004 WO 3

; CURRENT APPLICATION NUMBER: US/10/203,136  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 38578  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 38459  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
; FILE REFERENCE: EST\_HUMAN HIT: AUI17241.1, EVALUE 2.50e-01  
US-10-203-136-38459

Query Match 100.0%; Score 20; DB 26; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 3 DLDA 6

## RESULT 22

US-10-203-137-38679  
; Sequence 38679, Application US/10203137  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: PB 0004 WO 7  
; CURRENT APPLICATION NUMBER: US/10/203,137  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 38837  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 38679  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens

; FEATURE:  
; OTHER INFORMATION: MAP TO AL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2  
; FEATURE:  
; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUE 2.50e-01  
US-10-203-137-38679

Query Match 100.0%; Score 20; DB 26; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 3 DLDA 6

RESULT 23  
US-10-203-139-37058  
; Sequence 37058, Application US/10203139  
; GENERAL INFORMATION:  
; APPLICANT: Molecular Dynamics, Inc.  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER  
; FILE REFERENCE: PB 0004 WO 4  
; CURRENT APPLICATION NUMBER: US/10/203.139  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
; NUMBER OF SEQ ID NOS: 37156  
; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
; SEQ ID NO 37058  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL133246.1  
; FEATURE:  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9  
; FEATURE:  
; OTHER INFORMATION: EST\_HUMAN HIT: AU117241.1, EVALUE 2.50e-01  
US-10-203-139-37058

Query Match 100.0%; Score 20; DB 26; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 3 DLDA 6

RESULT 24  
US-09-512-563-43  
; Sequence 43, Application US/09512563  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan

; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-A  
; CURRENT APPLICATION NUMBER: US/09/512,563  
; CURRENT FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived  
; OTHER INFORMATION: peptide  
US-09-512-563-43

Query Match 100.0%; Score 20; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 7 DLDA 10

RESULT 25  
US-09-512-563A-43  
; Sequence 43, Application US/09512563A  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-A  
; CURRENT APPLICATION NUMBER: US/09/512,563A  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived  
; OTHER INFORMATION: peptide  
US-09-512-563A-43

Query Match 100.0%; Score 20; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 7 DLDA 10

RESULT 26  
US-09-512-563C-43  
; Sequence 43, Application US/09512563C  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-A  
; CURRENT APPLICATION NUMBER: US/09/512,563C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived  
; OTHER INFORMATION: peptide  
US-09-512-563C-43

Query Match 100.0%; Score 20; DB 19; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|||  
Db 7 DLDA 10

RESULT 27

US-07-698-925A-1  
; Sequence 1, Application US/07698925A  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Hong-Ji,  
; APPLICANT: Benedict, William F.,  
; APPLICANT: Hu, Shi-Xue  
; TITLE OF INVENTION: Retinoblastoma Protein Immunochemical  
; TITLE OF INVENTION: Retinoblastoma Protein Immunochemical  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Vaden, Eickenroht, Thompson & Boulware  
; STREET: One Riverway  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77056-1903  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/698,925A  
; FILING DATE: 19910513  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER:  
; APPLICATION NUMBER: US 07/338,289, US 07/508,051  
; FILING DATE: 14-APR-1989, 11-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Boulware, Margaret A.  
; REGISTRATION NUMBER: 28708  
; REFERENCE/DOCKET NUMBER: BAYAO08CIP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 961-3525  
; TELEFAX: (713) 961-3723  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
; FEATURE:  
; NAME/KEY: EXON 10 region - retinoblastoma protein  
; LOCATION: 322 - 341  
; OTHER INFORMATION: epitope of retinoblastoma protein  
US-07-698-925A-1

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|||  
Db 9 DLDA 12

RESULT 28

US-08-944-147-22  
; Sequence 22, Application US/08944147

; GENERAL INFORMATION:  
; APPLICANT: Jackson, David C.  
; APPLICANT: O'Brien-Simpson, Neil M.  
; APPLICANT: Brown, Lorena E.  
; APPLICANT: Ede, Nicholas J.  
; APPLICANT: Brandy, Evelyn R.  
; APPLICANT: Good, Michael F.  
; APPLICANT: Zeng, Weiquang  
; TITLE OF INVENTION: POLYMERS INCORPORATION PEPTIDES  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,147  
; FILING DATE: 06-OCT-1997  
; CLASSIFICATION: 526  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMillian, Nabeela R.  
; REGISTRATION NUMBER: P-43,363  
; REFERENCE/DOCKET NUMBER: FBRC:006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512)418-3000  
; TELEFAX: (512)474-7544  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-944-147-22

Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|||  
Db 4 DLDA 7

RESULT 29

US-08-944-147-22  
; Sequence 22, Application US/08944147A  
; GENERAL INFORMATION:  
; APPLICANT: JACKSON, DAVID C.  
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.  
; APPLICANT: BROWN, LORENA E.  
; APPLICANT: EDE, NICHOLAS J.  
; APPLICANT: BRANDT, EVELYN R.  
; APPLICANT: GOOD, MICHAEL F.  
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES  
; FILE REFERENCE: FBRC:006  
; CURRENT APPLICATION NUMBER: US/08/944,147A  
; CURRENT FILING DATE: 1997-10-06  
; EARLIER APPLICATION NUMBER: P05071  
; EARLIER FILING DATE: 1997-02-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:



; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-08-944-147-22

Query Match 100.0%; Score 20; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
Db 4 DLDA 7

## RESULT 30

US-10-044-034-22  
; Sequence 22, Application US/10044034  
; GENERAL INFORMATION:  
; APPLICANT: JACKSON, DAVID C.  
; APPLICANT: O'BRIEN-SIMPSON, NEIL M.  
; APPLICANT: BROWN, LORENA E.  
; APPLICANT: EDE, NICHOLAS J.  
; APPLICANT: BRANDT, EVELYN R.  
; APPLICANT: GOOD, MICHAEL F.  
; TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES  
; FILE REFERENCE: FBRC:006  
; CURRENT APPLICATION NUMBER: US/10/044,034  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: P05071  
; PRIOR FILING DATE: 1997-02-11  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-044-034-22

Query Match 100.0%; Score 20; DB 24; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
Db 4 DLDA 7

## RESULT 31

US-07-946-304-2  
; Sequence 2, Application US/07946304  
; GENERAL INFORMATION:  
; APPLICANT: Fung, Y.K.  
; TITLE OF INVENTION: Cell-Cycle-Dependent Regulation of  
; TITLE OF INVENTION: Phosphorylation of the Human Retinoblastoma Gene Product  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gray Cary Ware & Freidenrich  
; STREET: 401 "B" Street, Suite 1700  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/946,304  
; FILING DATE: 11-NOV-1992  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: Brotman, Harris F.  
; REGISTRATION NUMBER: 35,461  
; REFERENCE/DOCKET NUMBER: P00050USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-699-3630  
; TELEFAX: 619-236-1048  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 2..21  
; OTHER INFORMATION: /note= "Corresponds to amino acids  
; OTHER INFORMATION: 322 to 341 in Sequence ID No. 1"  
US-07-946-304-2

Query Match 100.0%; Score 20; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
| | | |  
Db 10 DLDA 13

## RESULT 32

US-07-969-314A-10  
; Sequence 10, Application US/07969314A  
; GENERAL INFORMATION:  
; APPLICANT: ROOS, Maria H.  
; TITLE OF INVENTION: SPECIFIC DNA SEQUENCE OF A NEMATODE  
; TITLE OF INVENTION: WHICH CAN BE USED FOR THE DIAGNOSIS OF INFECTION WITH TH  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: YOUNG & THOMPSON  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: US  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/969,314A  
; FILING DATE: 15-APR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: NL 9001832  
; FILING DATE: 16-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/NL91/00153  
; FILING DATE: 15-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE/DOCKET NUMBER: B036107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 521-2297  
; TELEFAX: (703) 685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-969-314A-10

Query Match      100.0%; Score 20; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    |||
Db 9 DLDA 12

RESULT 33
US-09-080-428-9
; Sequence 9, Application US/09080428
; GENERAL INFORMATION:
; APPLICANT: Golightly, Elizabeth,
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,428
; FILING DATE: 18-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Starnes, Robert L.
; REGISTRATION NUMBER: 41,324
; REFERENCE/DOCKET NUMBER: 5556,000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
US-09-080-428-9

Query Match      100.0%; Score 20; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
    |||
Db 8 DLDA 11

RESULT 34
US-09-724-059-530377
; Sequence 9, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 530377
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-530378
; Sequence 530378, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 530378
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide sequence
US-09-724-059-530378

Query Match      100.0%; Score 20; DB 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 DLDA 4
    |||
Db 14 DLDA 17

RESULT 36
US-09-724-059-530379
; Sequence 530379, Application US/09724059
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Isalan, Mark
; TITLE OF INVENTION: Nucleic Acid Binding Proteins
; FILE REFERENCE: P2500USM
; CURRENT APPLICATION NUMBER: US/09/724,059
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB9710809.6
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 1407122
; SOFTWARE: MacAllister
; SEQ ID NO 530379

```

; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-530379

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 37  
US-09-724-059-535338  
; Sequence 535338, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: MacAllister  
; SEQ ID NO 535338  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-535338

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 38  
US-09-724-059-538495  
; Sequence 538495, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: MacAllister  
; SEQ ID NO 538495  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-538495

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 39  
US-09-724-059-538496  
; Sequence 538496, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: MacAllister  
; SEQ ID NO 538496  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-538496

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 40  
US-09-724-059-559241  
; Sequence 559241, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: MacAllister  
; SEQ ID NO 559241  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559241

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 14 DLDA 17

RESULT 41  
US-09-724-059-559242

; Sequence 559242, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: Macallister  
; SEQ ID NO 559242  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559242

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
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Db 14 DLDA 17

## RESULT 42

US-09-724-059-559243  
; Sequence 559243, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: Macallister  
; SEQ ID NO 559243  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559243

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 14 DLDA 17

## RESULT 43

US-09-724-059-559244  
; Sequence 559244, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: Macallister  
; SEQ ID NO 559244  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559244

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 14 DLDA 17

## RESULT 44

US-09-724-059-559245  
; Sequence 559245, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: Macallister  
; SEQ ID NO 559245  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559245

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
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|  
Db 14 DLDA 17

## RESULT 45

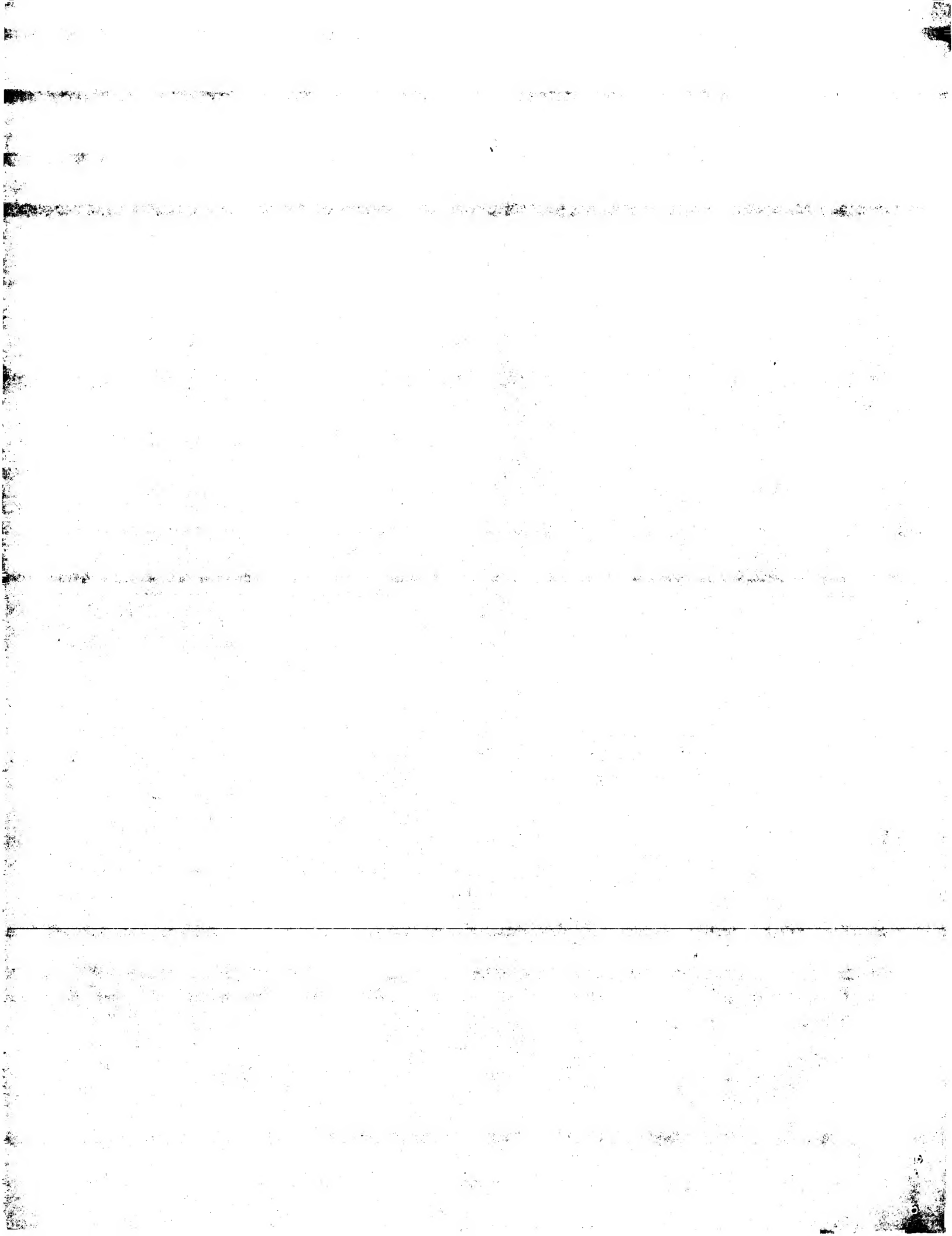
US-09-724-059-559246  
; Sequence 559246, Application US/09724059  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Isalan, Mark  
; TITLE OF INVENTION: Nucleic Acid Binding Proteins  
; FILE REFERENCE: P2500USM  
; CURRENT APPLICATION NUMBER: US/09/724,059  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; NUMBER OF SEQ ID NOS: 1407122  
; SOFTWARE: Macallister  
; SEQ ID NO 559246  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:

; OTHER INFORMATION: Polypeptide sequence  
US-09-724-059-559246

Query Match 100.0%; Score 20; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
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|  
Db 14 DLDA 17

Search completed: February 6, 2003, 11:37:32  
Job time : 135.167 secs



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# OM protein - protein search, using sw model

Run on: February 6, 2003, 11:19:49 ; Search time 14 seconds  
(without alignments)  
23.165 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dllda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 1507

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

## Database :

Pending\_Patents\_AA\_New.\*  
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2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	15	6	US-10-169-026-14
2	20	100.0	18	1	PCT-US02-00667A-95
3	20	100.0	19	6	US-10-270-837-43
4	20	100.0	19	6	US-10-270-877-43
5	20	100.0	33	5	US-09-684-758-9
6	20	100.0	33	5	US-09-684-758-11
7	20	100.0	33	5	US-09-684-758-13
8	20	100.0	33	5	US-09-684-758-15
9	20	100.0	50	5	US-09-492-935C-2
10	20	100.0	51	1	PCT-US02-32727-25319
11	20	100.0	51	6	US-10-057-498-25319
12	20	100.0	53	1	PCT-US02-32727-4206
13	20	100.0	53	6	US-10-057-498-4206
14	20	100.0	57	1	PCT-US02-32727-18426
15	20	100.0	57	5	US-09-513-999C-5509
16	20	100.0	57	6	US-10-057-498-18426
17	20	100.0	61	1	PCT-US02-32727-18873
18	20	100.0	61	5	US-09-950-084-5891
19	20	100.0	61	6	US-10-057-498-18873
20	20	100.0	64	1	PCT-US02-32727-488
21	20	100.0	64	6	US-10-057-498-488
22	20	100.0	72	1	PCT-US02-32727-22782
23	20	100.0	72	6	US-10-270-837-48
24	20	100.0	72	6	US-10-270-837-52
25	20	100.0	72	6	US-10-270-837-61
26	20	100.0	72	6	US-10-270-877-48

## ALIGNMENTS

### RESULT 1

US-10-169-026-14  
; Sequence 14, Application US/10169026  
; GENERAL INFORMATION:  
; APPLICANT: SATO, Atsushi  
; TITLE OF INVENTION: Cytokine-Like Peptide  
; FILE REFERENCE: 1254-0209P  
; CURRENT APPLICATION NUMBER: US/10/169,026  
; CURRENT FILING DATE: 2002-11-04  
; PRIOR APPLICATION NUMBER: JP 369990/1999  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09278  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 14  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide SYR6-N14  
US-10-169-026-14

Query Match 100.0%; Score 20; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db 11 DLDA 14

### RESULT 2

PCT-US02-00667A-95  
; Sequence 95, Application PC/TUS0200667A  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF MARYLAND, COLLEGE PARK  
; TITLE OF INVENTION: METHODS FOR DETERMINING RING NUMBER IN CAROTENOIDS BY  
; FILE REFERENCE: 108172-00055  
; CURRENT APPLICATION NUMBER: PCT/US02/00667A  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 60/261,473  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 18

Sequence 52, Appl  
Sequence 61, Appl  
Sequence 22782, A  
Sequence 22479, A  
Sequence 22479, A  
Sequence 5464, Ap  
Sequence 10139, A  
Sequence 6393, Ap  
Sequence 10139, A  
Sequence 18061, A  
Sequence 23116, A  
Sequence 18061, A  
Sequence 23116, A  
Sequence 17661, A  
Sequence 17661, A  
Sequence 4519, Ap  
Sequence 4519, Ap  
Sequence 26672, A

27 20 100.0 72 6 US-10-270-877-52  
28 20 100.0 72 6 US-10-270-877-61  
29 20 100.0 72 6 US-10-057-498-22782  
30 20 100.0 73 1 PCT-US02-32727-22479  
31 20 100.0 73 6 US-10-057-498-22479  
32 20 100.0 74 5 US-09-513-999C-5464  
33 20 100.0 74 5 US-09-513-999C-5490  
34 20 100.0 77 1 PCT-US02-32727-10139  
35 20 100.0 77 5 US-09-513-999C-6393  
36 20 100.0 77 6 US-10-057-498-10139  
37 20 100.0 78 1 PCT-US02-32727-18061  
38 20 100.0 78 1 PCT-US02-32727-23116  
39 20 100.0 78 6 US-10-057-498-18061  
40 20 100.0 78 6 US-10-057-498-23116  
41 20 100.0 79 1 PCT-US02-32727-17661  
42 20 100.0 79 6 US-10-057-498-17661  
43 20 100.0 81 5 US-09-134-000C-4519  
44 20 100.0 81 5 US-09-134-000C-4519  
45 20 100.0 83 1 PCT-US02-32727-26672

; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
PCT-US02-00667A-95

Query Match 100.0%; Score 20; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 13 DLDA 16

## RESULT 3

US-10-270-837-43  
; Sequence 43, Application US/10270837  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD2  
; CURRENT APPLICATION NUMBER: US/10/270,837  
; PRIOR FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived  
US-10-270-837-43

Query Match 100.0%; Score 20; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 7 DLDA 10

## RESULT 4

US-10-270-877-43  
; Sequence 43, Application US/10270877  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD1  
; CURRENT APPLICATION NUMBER: US/10/270,877  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPIII derived  
US-10-270-877-43

Query Match 100.0%; Score 20; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 7 DLDA 10

## RESULT 5

US-09-684-758-9  
; Sequence 9, Application US/09684758  
; GENERAL INFORMATION:  
; APPLICANT: Bjorck, Lars H.  
; APPLICANT: Frick, Inga-Maria  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: 100084.413US  
; CURRENT APPLICATION NUMBER: US/09/684,758  
; CURRENT FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
US-09-684-758-9

Query Match 100.0%; Score 20; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 28 DLDA 31

## RESULT 6

US-09-684-758-11  
; Sequence 11, Application US/09684758  
; GENERAL INFORMATION:  
; APPLICANT: Bjorck, Lars H.  
; APPLICANT: Frick, Inga-Maria  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: 100084.413US  
; CURRENT APPLICATION NUMBER: US/09/684,758  
; CURRENT FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
US-09-684-758-11

Query Match 100.0%; Score 20; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 28 DLDA 31

## RESULT 7

US-09-684-758-13  
; Sequence 13, Application US/09684758  
; GENERAL INFORMATION:  
; APPLICANT: Bjorck, Lars H.  
; APPLICANT: Frick, Inga-Maria  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: 100084.413US  
; CURRENT APPLICATION NUMBER: US/09/684,758  
; CURRENT FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 13



; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
US-09-684-758-13

Query Match 100.0%; Score 20; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 28 DLDA 31

RESULT 8  
US-09-684-758-15  
; Sequence 15, Application US/09684758  
; GENERAL INFORMATION:  
; APPLICANT: Bjorck, Lars H.  
; APPLICANT: Frick, Inga-Maria  
; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: 100084.413US  
; CURRENT APPLICATION NUMBER: US/09/684,758  
; CURRENT FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
US-09-684-758-15

Query Match 100.0%; Score 20; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 28 DLDA 31

RESULT 9  
US-09-492-935C-2  
; Sequence 2, Application US/09492935C  
; GENERAL INFORMATION:  
; APPLICANT: STEM CELL PHARMACEUTICALS, INC.  
; APPLICANT: TWARDZIK, Daniel  
; APPLICANT: PERNET, Andre  
; APPLICANT: FELKER, Thomas S.  
; APPLICANT: PASKELL, Stefan  
; TITLE OF INVENTION: USES OF TGF-alpha AND RELATED POLYPEPTIDES  
; FILE REFERENCE: STEM1110-1  
; CURRENT APPLICATION NUMBER: US/09/492,935C  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 09/378,567  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 50  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-492-935C-2

Query Match 100.0%; Score 20; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 47 DLDA 50

RESULT 10  
PCT-US02-32727-25319  
; Sequence 25319, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 25319  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-25319

Query Match 100.0%; Score 20; DB 1; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 20 DLDA 23

RESULT 11  
US-10-057-498-25319  
; Sequence 25319, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057.498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 25319  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-25319

Query Match 100.0%; Score 20; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 20 DLDA 23

RESULT 12  
PCT-US02-32727-4206  
; Sequence 4206, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siging  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 4206  
; LENGTH: 53  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-4206

Query Match 100.0%; Score 20; DB 1; Length 53;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 13 DLDA 16

RESULT 13  
US-10-057-498-4206  
; Sequence 4206, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 4206  
; LENGTH: 53  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-4206

Query Match 100.0%; Score 20; DB 6; Length 53;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 13 DLDA 16

RESULT 14  
PCT-US02-32727-18426  
; Sequence 18426, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siging  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 18426  
; LENGTH: 57  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-18426

Query Match 100.0%; Score 20; DB 1; Length 57;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 12 DLDA 15

RESULT 15  
US-09-513-999C-5509  
; Sequence 5509, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5509  
; LENGTH: 57  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: UNSURE  
; LOCATION: 43  
; OTHER INFORMATION: Xaa-Lys or Thr  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 44  
; OTHER INFORMATION: Xaa-Lys or Gln  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 45  
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 46  
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 48  
; OTHER INFORMATION: Xaa-Ile or Lys or Arg or Thr  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 50  
; OTHER INFORMATION: Xaa-Glu or Lys  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 51  
; OTHER INFORMATION: Xaa-Gln or Arg  
US-09-513-999C-5509

Query Match 100.0%; Score 20; DB 5; Length 57;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 18 DLDA 21

## RESULT 16

US-10-057-498-18426  
; Sequence 18426, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 18426  
; LENGTH: 57  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-18426

Query Match 100.0%; Score 20; DB 6; Length 57;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 12 DLDA 15

## RESULT 17

PCT-US02-32727-18873  
; Sequence 18873, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 18873  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-18873

Query Match 100.0%; Score 20; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 13 DLDA 16

## RESULT 18

US-09-950-084-5891  
; Sequence 5891, Application US/09950084  
; GENERAL INFORMATION:  
; APPLICANT: George H. Shimer, Jr.  
; APPLICANT: George H. Miller  
; APPLICANT: Roberta S. Hare  
; APPLICANT: Karen J. Shaw  
; TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods  
; FILE REFERENCE: 1034/1C963US2  
; CURRENT APPLICATION NUMBER: US/09/950,084  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US 09/417,811  
; PRIOR FILING DATE: 1999-10-14  
; PRIOR APPLICATION NUMBER: US 09/353,718  
; PRIOR FILING DATE: 1999-07-14  
; PRIOR APPLICATION NUMBER: US 09/266,557  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 09/266,556  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 09/266,555  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 09/266,542  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 09/266,541  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 09/037,934  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 09/036,720  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: US 09/036,338  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 7451  
; SEQ ID NO 5891  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-950-084-5891

Query Match 100.0%; Score 20; DB 5; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 17 DLDA 20

## RESULT 19

US-10-057-498-18873  
; Sequence 18873, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 18873  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-18873

Query Match 100.0%; Score 20; DB 6; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
      ||||  
Db 13 DLDA 16

RESULT 20  
PCT-US02-32727-488  
; Sequence 488, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Fanni  
; APPLICANT: Wang, Shiqing  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 488  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-488

Query Match 100.0%; Score 20; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 47 DLDA 50

RESULT 21  
US-10-057-498-488  
; Sequence 488, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 488  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-488

Query Match 100.0%; Score 20; DB 6; Length 64;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 47 DLDA 50

RESULT 22  
PCT-US02-32727-22782  
; Sequence 22782, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Fanni  
; APPLICANT: Wang, Shiqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 22782  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-22782

Query Match 100.0%; Score 20; DB 1; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 62 DLDA 65

RESULT 23  
US-10-270-837-48  
; Sequence 48, Application US/10270837  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD2  
; CURRENT APPLICATION NUMBER: US/10/270,837  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPDIII  
US-10-270-837-48

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

RESULT 24  
US-10-270-837-52  
; Sequence 52, Application US/10270837  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD2  
; CURRENT APPLICATION NUMBER: US/10/270,837  
; CURRENT FILING DATE: 2002-10-11

; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPDIII-V  
US-10-270-837-52

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

## RESULT 25

US-10-270-837-61  
; Sequence 61, Application US/10270837  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD2  
; CURRENT APPLICATION NUMBER: US/10/270,837  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-270-837-61

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

## RESULT 26

US-10-270-877-48  
; Sequence 48, Application US/10270877  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD1  
; CURRENT APPLICATION NUMBER: US/10/270,877  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
;

; OTHER INFORMATION: Description of Artificial Sequence: GPDIII  
US-10-270-877-48

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

## RESULT 27

US-10-270-877-52  
; Sequence 52, Application US/10270877  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD1  
; CURRENT APPLICATION NUMBER: US/10/270,877  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: GPDIII-V  
US-10-270-877-52

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

## RESULT 28

US-10-270-877-61  
; Sequence 61, Application US/10270877  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Goodpasture Binding Protein  
; FILE REFERENCE: 98-723-AD1  
; CURRENT APPLICATION NUMBER: US/10/270,877  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 09/512,563  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/121,483  
; PRIOR FILING DATE: 1999-02-24  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 72  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-270-877-61

Query Match 100.0%; Score 20; DB 6; Length 72;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

```
RESULT 29
US-10-057-498-22782
; Sequence 22782, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 22782
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-22782

Query Match          100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 62 DLDA 65

RESULT 30
PCT-US02-32727-22479
; Sequence 22479, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 22479
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-22479

Query Match          100.0%; Score 20; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 60 DLDA 63

RESULT 31
US-10-057-498-22479
; Sequence 22479, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 22782
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-22782

Query Match          100.0%; Score 20; DB 6; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 62 DLDA 65

RESULT 32
US-09-513-999C-5464
; Sequence 5464, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5464
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: UNSURE
; LOCATION: 7
; OTHER INFORMATION: Xaa-Arg or Thr
US-09-513-999C-5464

Query Match          100.0%; Score 20; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 31 DLDA 34

RESULT 33
US-09-513-999C-5490
; Sequence 5490, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5490
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5490
```

; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 56  
; OTHER INFORMATION: Xaa=Lys or Asn  
US-09-513-999C-5490

Query Match 100.0%; Score 20; DB 5; Length 74;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 60 DLDA 63

RESULT 34  
PCT-US02-32727-10139

; Sequence 10139, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 10139  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-10139

Query Match 100.0%; Score 20; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 70 DLDA 73

RESULT 35  
US-09-513-999C-6393

; Sequence 6393, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6393  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: UNSURE  
; LOCATION: 66  
; OTHER INFORMATION: Xaa-His or Leu or Pro or Arg  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 72  
; OTHER INFORMATION: Xaa=Gly or Val  
US-09-513-999C-6393

Query Match 100.0%; Score 20; DB 5; Length 77;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 3 DLDA 6

RESULT 36

US-10-057-498-10139  
; Sequence 10139, Application US/10057498  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 10139  
; LENGTH: 77  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-10139

Query Match 100.0%; Score 20; DB 6; Length 77;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 70 DLDA 73

RESULT 37

PCT-US02-32727-18061  
; Sequence 18061, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 18061  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-18061

Query Match 100.0%; Score 20; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
      ||||  
Db 42 DLDA 45

## RESULT 38

PCT-US02-32727-23116  
; Sequence 23116, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Siging

; APPLICANT: Jen, Shyian

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 23116

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-23116

Query Match 100.0%; Score 20; DB 1; Length 78;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
      ||||  
Db 67 DLDA 70

## RESULT 39

US-10-057-498-18061

; Sequence 18061, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 18061

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-18061

Query Match 100.0%; Score 20; DB 6; Length 78;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
      ||||  
Db 42 DLDA 45

## RESULT 40

US-10-057-498-23116

; Sequence 23116, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A

; FILE REFERENCE: 210121.514

; CURRENT APPLICATION NUMBER: US/10/057,498

; CURRENT FILING DATE: 2001-04-20

; NUMBER OF SEQ ID NOS: 29212

; SEQ ID NO 23116

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Propioni acnes

US-10-057-498-23116

Query Match 100.0%; Score 20; DB 6; Length 78;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

      ||||

Db 67 DLDA 70

## RESULT 41

PCT-US02-32727-17661

; Sequence 17661, Application PC/TUS0232727

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir

; APPLICANT: Persing, David

; APPLICANT: Bhatia, Ajay

; APPLICANT: Maisonneuve, Jean Francois

; APPLICANT: Zhang, Yanni

; APPLICANT: Wang, Siging

; APPLICANT: Jen, Shyian

; APPLICANT: Lodes, Michael

; APPLICANT: Benson, Darin

; APPLICANT: Jones, Robert

; APPLICANT: Carter, Darrick

; APPLICANT: Barth, Brenda

; APPLICANT: Douglass, John

; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A

; FILE REFERENCE: 210121.514C1

; CURRENT APPLICATION NUMBER: PCT/US02/32727

; CURRENT FILING DATE: 2002-10-11

; NUMBER OF SEQ ID NOS: 30992

; SEQ ID NO 17661

; LENGTH: 79

; TYPE: PRT

; ORGANISM: Propioni acnes

PCT-US02-32727-17661

Query Match 100.0%; Score 20; DB 1; Length 79;

Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

      ||||

Db 37 DLDA 40

## RESULT 42

US-10-057-498-17661

; Sequence 17661, Application US/10057498

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer

; APPLICANT: Skeiky, Yasir



; APPLICANT: Persing, David  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes  
; FILE REFERENCE: 210121.514  
; CURRENT APPLICATION NUMBER: US/10/057,498  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 29212  
; SEQ ID NO 17661  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
US-10-057-498-17661

Query Match 100.0%; Score 20; DB 6; Length 79;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 37 DLDA 40

RESULT 43  
US-09-134-000C-4519  
; Sequence 4519, Application US/09134000C  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4519  
; LENGTH: 81  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4519

Query Match 100.0%; Score 20; DB 5; Length 81;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 54 DLDA 57

RESULT 44  
US-09-134-000C-4519  
; Sequence 4519, Application US/09134000C  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4519  
; LENGTH: 81  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4519

Query Match 100.0%; Score 20; DB 5; Length 81;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 54 DLDA 57

RESULT 45  
PCT-US02-32727-26672  
; Sequence 26672, Application PC/TUS0232727  
; GENERAL INFORMATION:  
; APPLICANT: Mitcham, Jennifer  
; APPLICANT: Skeiky, Yasir  
; APPLICANT: Persing, David  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Maisonneuve, Jean Francois  
; APPLICANT: Zhang, Yanni  
; APPLICANT: Wang, Siqing  
; APPLICANT: Jen, Shyian  
; APPLICANT: Lodes, Michael  
; APPLICANT: Benson, Darin  
; APPLICANT: Jones, Robert  
; APPLICANT: Carter, Darrick  
; APPLICANT: Barth, Brenda  
; APPLICANT: Douglass, John  
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of A  
; FILE REFERENCE: 210121.514C1  
; CURRENT APPLICATION NUMBER: PCT/US02/32727  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 30992  
; SEQ ID NO 26672  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Propioni acnes  
PCT-US02-32727-26672

Query Match 100.0%; Score 20; DB 1; Length 83;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 9 DLDA 12

Search completed: February 6, 2003, 11:39:01  
Job time : 15 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:04 ; Search time 10.5 seconds  
(without alignments)  
36.623 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2360

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	26	2	PL0027
2	20	100.0	28	2	S15235
3	20	100.0	57	2	D44530
4	20	100.0	60	2	H41476
5	20	100.0	61	2	A36916
6	20	100.0	66	2	T35138
7	20	100.0	69	2	D86682
8	20	100.0	70	2	C86462
9	20	100.0	71	1	H70799
10	20	100.0	72	2	D86570
11	20	100.0	72	2	A72055
12	20	100.0	74	2	D95048
13	20	100.0	74	2	B97919
14	20	100.0	75	2	T17107
15	20	100.0	76	2	T25085
16	20	100.0	77	2	C95004
17	20	100.0	77	2	F97876
18	20	100.0	79	2	S38756
19	20	100.0	79	2	C87558
20	20	100.0	79	2	B64614
21	20	100.0	79	2	C71901
22	20	100.0	80	2	A90957
23	20	100.0	80	2	H75472
24	20	100.0	80	2	E85805
25	20	100.0	81	2	A49736
26	20	100.0	82	2	F75326
27	20	100.0	84	2	E84345
28	20	100.0	84	2	B97300
29	20	100.0	85	2	A70898

30 20 100.0 86 2 C95304  
31 20 100.0 87 2 F40361  
32 20 100.0 87 2 T43570  
33 20 100.0 87 2 H70079  
34 20 100.0 87 2 AF3030  
35 20 100.0 91 2 E90766  
36 20 100.0 91 2 F85716  
37 20 100.0 92 2 E83305  
38 20 100.0 92 2 JC4564  
39 20 100.0 93 2 E83630  
40 20 100.0 94 2 AC3252  
41 20 100.0 95 2 S24146  
42 20 100.0 96 2 S71519  
43 20 100.0 96 2 H83065  
44 20 100.0 97 2 H98254  
45 20 100.0 98 2 S61079

#### ALIGNMENTS

##### RESULT 1

PL0027

M protein pepM19 - Streptococcus sp. (fragment)

C:Species: Streptococcus sp.

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Feb-1997

C:Accession: PL0027

R:Bronze, M.S.; Beachey, E.H.; Dale, J.B.

J. Exp. Med. 167, 1849-1859, 1988

A:Title: Protective and heart-crossreactive epitopes located within the NH2 terminu

A:Reference number: PL0027; MUID:88258373; PMID:2455015

A:Accession: PL0027

A:Molecule type: protein

A:Residues: 1-26 <BRO>

C:Superfamily: M5 protein

C:Keywords: virulence factor

Query Match 100.0%; Score 20; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 95;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 18 DLDA 21

##### RESULT 2

S15235

hypothetical protein - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 08-Oct-1999

C:Accession: S15235

R:Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.

Mol. Microbiol. 5, 163-171, 1991

A:Title: Molecular characterization of the gor gene encoding glutathione reductase

A:Reference number: S15235; MUID:91194546; PMID:1849605

A:Accession: S15235

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-28 <PER>

A:Cross-references: EMBL:X54201; NID:g45324; PIDN:CAA38121.1; PID:g45325

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 28;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 14 DLDA 17

##### RESULT 3

D44530  
T-cell receptor alpha chain V region (BTA40) - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: D44530  
R:Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A:Reference number: A45893; MUID:90129157; PMID:2137108  
A:Accession: D44530  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-57 <ISH>  
A:Cross-references: GB:D90022; NID:g217632; PIDN:BAAL4072.1; PID:g217633  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 100.0%; Score 20; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 1 DLDA 4

RESULT 4  
H41476  
probable antigen 8 - Mycobacterium leprae (fragment)  
C:Species: Mycobacterium leprae  
C:Date: 10-Apr-1992 #sequence\_revision 10-Apr-1992 #text\_change 18-Jun-1993  
C:Accession: H41476  
R:Hartsekerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.  
Infect. Immun. 58, 2821-2827, 1990  
A:Title: Selection and characterization of recombinant clones that produce Mycobacterium  
A:Reference number: A41476; MUID:90354041; PMID:1696931  
A:Accession: H41476  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-60 <HAR>

Query Match 100.0%; Score 20; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 45 DLDA 48

RESULT 5  
A36916  
orf61 5' of int - Streptomyces lividans.  
C:Species: Streptomyces lividans  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
C:Accession: A36916  
R:Brasch, M.A.; Pettis, G.S.; Lee, S.C.; Cohen, S.N.  
J. Bacteriol. 175, 3067-3074, 1993  
A:Title: Localization and nucleotide sequences of genes mediating site-specific recombination  
A:Reference number: A36916; MUID:93259953; PMID:8387993  
A:Accession: A36916  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-61 <BRA>  
A>Note: sequence extracted from NCBI backbone (NCBIN:131954, NCBI:P:131955)

Query Match 100.0%; Score 20; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 49 DLDA 52

#### RESULT 6

T35138  
hypothetical protein SC4H8.07c SC4H8.07c - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C:Accession: T35138  
R:Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, December 1997  
A:Reference number: Z21569  
A:Accession: T35138  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-66 <HAR>  
A:Cross-references: EMBL:AL020958; PIDN:CAAL5874.1; GSPDB:GN00070; SCOEDB:SC4H8.07c  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC4H8.07c

Query Match 100.0%; Score 20; DB 2; Length 66;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 7 DLDA 10

#### RESULT 7

D86682  
prophage pil protein 25 [imported] - Lactococcus lactis subsp. lactis (strain IL140  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: D86682  
R:Botolin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Welissenbach, J.;  
Genome Res. 11, 751-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lact  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: D86682  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-69 <STO>  
A:Cross-references: GB:AE005176; PID:g12723339; PIDN:AAK04558.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: pil25

Query Match 100.0%; Score 20; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
Db 41 DLDA 44

#### RESULT 8

C86462  
unknown protein, 62609-62906 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: C86462  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Ali-  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: C86462  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-70 <STO>  
 A:Cross-references: GB:AE005172; NID:g6957515; PIDN:AAF32437.1; GSPDB:GN00141  
 C:Genetics:  
 A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 ||||  
 DB 25 DLDA 28

## RESULT 9

H70799  
 Integrase-related protein - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: H70799

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: H70799  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
 A:Residues: 1-71 <COL>

A:Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18073.1; PID:g296017  
 A:Experimental source: strain H37RV

C:Genetics:  
 A:Gene: RV3751

C:Superfamily: Mycobacterium tuberculosis integrase-related protein

Query Match 100.0%; Score 20; DB 1; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 ||||  
 DB 55 DLDA 58

## RESULT 10

D86570  
 L29 ribosomal protein [imported] - Chlamydomophila pneumoniae (strain J138)  
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001  
 C:Accession: D86570

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishii, K. Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
 A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: D86570  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-72 <STO>

A:Cross-references: GB:BA000008; NID:g8979011; PIDN:BAA98846.1; GSPDB:GN00142  
 A:Experimental source: strain J138

C:Genetics:  
 A:Gene: r129

Query Match 100.0%; Score 20; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 ||||  
 DB 18 DLDA 21

## RESULT 11

A72055

ribosomal protein L29 CP0108 [imported] - Chlamydomophila pneumoniae (strains CWL029  
 C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
 C:Accession: A72055; H81611

R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood  
 Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
 A:Reference number: A72000; MUID:99206606; PMID:10192388

A:Accession: A72055  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-72 <ARN>

A:Cross-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAI8778.1; PID:g  
 A:Experimental source: strain CWL029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; H  
 ; C.; Dodson, R.; Giehn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Sal  
 Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae A

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: H81611  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-72 <REA>

A:Cross-references: GB:AE002173; GB:AE002161; NID:g7189033; PIDN:AAF37991.1; PID:g  
 A:Experimental source: strain AR39, HL cells

C:Genetics:  
 A:Gene: r129; CP0108

Query Match 100.0%; Score 20; DB 2; Length 72;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 ||||  
 DB 18 DLDA 21

## RESULT 12

D95048

acyl carrier protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
 C:Accession: D95048

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.  
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtz  
 nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor  
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: D95048  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-74 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK74581.1; PID:g14971887; GSPDB:GN00164; TI  
 A:Experimental source: strain TIGR4

C:Genetics:  
 A:Gene: SP0418

Query Match 100.0%; Score 20; DB 2; Length 74;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 ||||  
 DB 30 DLDA 33

```
RESULT 13
B97919
acyl carrier protein [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: B97919
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; F
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B97919
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-74 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99182.1; PID:g15457939; GSPDB:GN00174
C:Genetics:
A:Gene: acp

Query Match 100.0%; Score 20; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 30 DLDA 33

RESULT 14
T17107
proline rich protein - apple tree (fragment)
C:Species: Malus domestica (apple tree)
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C:Accession: T17107
R:Dong, Y.H.; Janssen, B.J.; Bielecki, L.L.; Atkinson, R.G.; Morris, B.A.; Gardner, R.C.
J. Am. Soc. Hort. Sci. 122, 752-757, 1997
A:Title: Isolating and characterizing genes differentially expressed early in apple fruit
A:Reference number: Z18681
A:Accession: T17107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-75 <DON>
A:Cross-references: EMBL:U80271; NID:g1732364; PID:g1732365
A:Experimental source: strain Granny Smith
C:Genetics:
A:Gene: PRP
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 100.0%; Score 20; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 31 DLDA 34

RESULT 15
T29085
hypothetical protein SCIC2.36 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T29085
R:Redenbach, M.; Kreser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
Mol. Microbiol. 21, 77-96, 1996
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb s
A:Reference number: Z20556; MUID:97000351; PMID:8843436
A:Accession: T29085
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-76 <RED>
A:Cross-references: EMBL:AL031124; NID:el1312893; PID:el1312929; PIDN:CAA20003.1
C:Genetics:
A:Note: SCIC2.36

Query Match 100.0%; Score 20; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 65 DLDA 68

RESULT 16
C95004
acyl carrier protein, probable [imported] - Streptococcus pneumoniae (strain TIGR4
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: C95004
R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtz
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95004
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK74228.1; PID:g14971502; GSPDB:GN00164; TIG
C:Genetics:
A:Gene: SP0038

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
Db 33 DLDA 36

RESULT 17
F97876
acyl carrier protein [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: F97876
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas,
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F97876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK98842.1; PID:g15457569; GSPDB:GN00174
C:Genetics:
A:Gene: acp

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
||||
```

Db 33 DLDA 36

RESULT 18  
S38756  
Cytochrome c551 - Ectothiorhodospira halochloris  
C:Species: Ectothiorhodospira halochloris  
C:Date: 19-May-1994 #sequence\_revision 19-Apr-1996 #text\_change 04-Mar-2000  
C:Accession: S38756  
R:Amblar, R.P.; Meyer, T.E.; Kamen, M.D.  
Arch. Biochem. Biophys. 306, 83-93, 1993  
A:Title: Amino acid sequences of cytochromes c-551 from the halophilic purple phototroph  
A:Reference number: S38755; MUID:94028993; PMID:8215425  
A:Accession: S38756  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-79 <AMB>  
C:Superfamily: cytochrome c6; cytochrome c6 homolog  
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein  
F:3-74/Domain: cytochrome c6 homolog <CYC>  
F:14.17/Binding site: heme (Cys) (covalent) #status predicted  
F:18.55/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 38 DLDA 41

RESULT 19  
C87558  
conserved hypothetical protein CC2492 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 17-May-2002  
C:Accession: C87558  
R:NIerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Leub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: C87558  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <STO>  
A:Cross-references: GB:AE005673; NID:g13424047; PIDN:AAK24463.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC2492  
C:Superfamily: conserved hypothetical protein MJ1593

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 45 DLDA 48

RESULT 20  
B64614  
hypothetical protein HP0754 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C:Accession: B64614  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

Db 33 DLDA 36

RESULT 18  
S38756  
Cytochrome c551 - Ectothiorhodospira halochloris  
C:Species: Ectothiorhodospira halochloris  
C:Date: 19-May-1994 #sequence\_revision 19-Apr-1996 #text\_change 04-Mar-2000  
C:Accession: S38756  
R:Amblar, R.P.; Meyer, T.E.; Kamen, M.D.  
Arch. Biochem. Biophys. 306, 83-93, 1993  
A:Title: Amino acid sequences of cytochromes c-551 from the halophilic purple phototroph  
A:Reference number: S38755; MUID:94028993; PMID:8215425  
A:Accession: S38756  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-79 <AMB>  
C:Superfamily: cytochrome c6; cytochrome c6 homolog  
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein  
F:3-74/Domain: cytochrome c6 homolog <CYC>  
F:14.17/Binding site: heme (Cys) (covalent) #status predicted  
F:18.55/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 38 DLDA 41

RESULT 19  
C87558  
conserved hypothetical protein CC2492 [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 17-May-2002  
C:Accession: C87558  
R:NIerman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Leub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: C87558  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <STO>  
A:Cross-references: GB:AE005673; NID:g13424047; PIDN:AAK24463.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC2492  
C:Superfamily: conserved hypothetical protein MJ1593

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 45 DLDA 48

RESULT 20  
B64614  
hypothetical protein HP0754 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C:Accession: B64614  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: B64614  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-79 <TOM>  
A:Cross-references: GB:AE000588; GB:AE000511; NID:g2313880; PIDN:AAD07810.1; PID:G

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 39 DLDA 42

RESULT 21  
C71901  
hypothetical protein jhp0691 - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
C:Accession: C71901  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith,  
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: C71901  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-79 <ARN>  
A:Cross-references: GB:AE001500; GB:AE001439; NID:g4155238; PIDN:AAD06266.1; PID:G  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: jhp0691

Query Match 100.0%; Score 20; DB 2; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 39 DLDA 42

RESULT 22  
A90957  
hypothetical protein ECS2625 [imported] - Escherichia coli (strain O157:H7, substr.  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: A90957  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 an  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: A90957  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-80 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BAH36048.1; PID:g13362093; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECS2625

Query Match 100.0%; Score 20; DB 2; Length 80;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||

Db 51 DLDA 54

RESULT 23

H75472

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000

C:Accession: H75472

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: H75472

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <WHI>

A:Cross-references: GB:AE001935; GB:AE000513; NID:g6458517; PIDN:AAF10390.1; PID:g645852

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0803

A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 41 DLDA 44

RESULT 24

E85805

unknown protein encoded by prophage CP-933T [imported] - Escherichia coli (strain O157:H

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

C:Accession: E85805

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85805

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-80 <STO>

A:Cross-references: GB:AE005174; NID:gl2515982; PIDN:AAG56905.1; GSPDB:GN00145; UWGP:Z29

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z2973

Query Match 100.0%; Score 20; DB 2; Length 80;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 51 DLDA 54

RESULT 25

A49736

collagen alpha 3(IV) chain, short splice form - human (fragment)

N:Contains: collagen alpha 3 (IV) chain, splice form GP-III

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence\_revision 12-Nov-1999 #text\_change 12-Nov-1999

C:Accession: A49736; C49736; B45971; S69112

R:Feng, L.; Xia, Y.; Wilson, C.B.

J. Biol. Chem. 269, 2342-2348, 1994

A:Title: Alternative splicing of the NCI domain of the human alpha3(IV) collagen gene. D

A:Reference number: A49736; MUID:94124597; PMID:8294492

A:Accession: A49736

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 71-81 <FEN1>

A:Accession: C49736

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 22-81 <FEN2>

A:Cross-references: GB:U02520; NID:g408895; PIDN:AAAI8943.1; PID:g408896

A:Note: This is the conceptual translation of the nucleic acid submitted to GenBank

R:Bernal, D.; Quinones, S.; Saus, J.

J. Biol. Chem. 268, 12090-12094, 1993

A:Title: The human mRNA encoding the Goodpasture antigen is alternatively spliced.

A:Reference number: A45971; MUID:93280184; PMID:8505332

A:Accession: B45971

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 71-81 <BER>

A:Cross-references: PIDN:AAE27014.1; PID:g385563

A:Note: sequence extracted from NCBI backbone (NCBIP:133955); sequence incorrectly

R:Penades, J.R.; Bernal, D.; Revert, F.; Johansson, C.; Fresquet, V.J.; Cervera, J. Eur. J. Biochem. 229, 754-760, 1995

A:Title: Characterization and expression of multiple alternatively spliced transcri

ptantigen and one of its alternative forms.

A:Reference number: S69111; MUID:95278230; PMID:7758473

A:Accession: S69112

A:Molecule type: mRNA

A:Residues: 1-45,71-81 <PEN>

C:Comment: For the complete sequence of the long splice form, see PIR:CGHU3B.

C:Genetics:

A:Gene: GDB:COL4A3

A:Cross-references: GDB:128351; OMIM:120070

A:Map position: 2q36-2q37

C:Superfamily: collagen alpha 1(IV) chain

C:Keywords: alternative splicing; basement membrane; cell binding; coiled coil; ext

F:1-81/Product: collagen alpha 3(IV) chain, short splice form (fragment) #status p

F:1-45,71-81/Product: collagen alpha 3 (IV) chain, splice form GP-III (fragment) #

F:22-81/Domain: carboxyl-terminal nonhelical, NCI <NCI>

Query Match 100.0%; Score 20; DB 2; Length 81;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4

||||

Db 69 DLDA 72

RESULT 26

F75326

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: F75326

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, J M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75326

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-82 <WHI>

A:Cross-references: GB:AE002038; NID:g6459790; PIDN:AAF11556.1; PID:g

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2009

A:Map position: 1

Query Match 100.0%; Score 20; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 75 DLDA 78

#### RESULT 27

E84345 hypothetical protein Vng1944c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: E84345

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: E84345

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-84 <STO>

A:Cross-references: GB:AE004437; NID:g10581384; PIDN:AAG20129.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG1944C

Query Match 100.0%; Score 20; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 47 DLDA 50

#### RESULT 28

B97300

hypothetical protein CAC3255 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C:Accession: B97300

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97300

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-84 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81189.1; PID:g15026329; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3255

Query Match 100.0%; Score 20; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 67 DLDA 70

#### RESULT 29

A70898

probable xseB protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: A70898

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrc  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete c

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70898

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-85 <COL>

A:Cross-references: GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA1723.1; PID:c

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: xseB

Query Match 100.0%; Score 20; DB 2; Length 85;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 44 DLDA 47

#### RESULT 30

C95304

hypothetical transposase, partial match [imported] - Sinorhizobium meliloti (strai

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C:Accession: C95304

R:Barrett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium m

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: C95304

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK64997.1; PID:g14523425; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-H

pla, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Le

hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Y

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

C:Contents: annotation

C:Genetics:

A:Gene: SMA0643

A:Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 86;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

Db 31 DLDA 34

#### RESULT 31

F40361

virC-region hypothetical protein yscF - Yersinia enterocolitica plasmid pyv

C:Species: Yersinia enterocolitica

C>Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 08-Oct-1999

C:Accession: F40361

R:Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvroit, C.; China, B.; Gustin, A.,

J. Bacteriol. 173, 4994-5009, 1991

A:Title: Analysis of virC, an operon involved in the secretion of Yop proteins by

A:Reference number: A40361; MUID:91317716; PMID:1860816

A:Accession: F40361  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-87 <MHC>  
A:Cross-references: GB:M74011; NID:g155549; PIDN:AAC37023.1; PID:g155555  
C:Genetics:  
A:Genome: plasmid

Query Match 100.0%; Score 20; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 15 DLDA 18

RESULT 32

T43570

type III secretion protein yscF - Yersinia pestis plasmid pCD1  
N:Alternate names: translocation protein F homolog  
C:Species: Yersinia pestis  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T43570; T42865  
R:Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998  
A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.  
A:Reference number: 222578; MUID:98422474; PMID:9748454

A:Accession: T43570  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <HUP>  
A:Cross-references: EMBL:AF053946; NID:g2996222; PIDN:AAC62549.1; PID:g2996226  
A:Experimental source: strain KIM  
R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998  
A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia F  
A:Reference number: 222273; MUID:98427122; PMID:9746557

A:Accession: T42865  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-87 <PER>  
A:Cross-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69778.1; PID:g3822058  
A:Experimental source: strain KIM5  
C:Genetics:  
A:Gene: yscF  
A:Genome: plasmid pCD1

Query Match 100.0%; Score 20; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 15 DLDA 18

RESULT 33

H70079  
hypothetical protein yxjJ - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 21-Jul-2000  
C:Accession: H70079  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chhabria, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; akeuchi, M.; Tamakoshi, A.; Tanaka, P.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchi, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshi, A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: H70079  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-87 <KUN>  
A:Cross-references: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CAB15919.1; PID:g26:  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yxjJ

Query Match 100.0%; Score 20; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 74 DLDA 77

RESULT 34

AF3030  
hypothetical protein Atu3850 [imported] - Agrobacterium tumefaciens (strain C58, D  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
C:Accession: AF3030  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; M: Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; PMID:11743193  
A:Accession: AF3030  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-87 <KUR>  
A:Cross-references: GB:AE008689; PIDN:AAL44660.1; PID:g17742285; GSPDB:GN00187  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3850  
A:Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 87;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4

||||

Db 35 DLDA 38

RESULT 35

E90766  
hypothetical protein Ecs1101 [imported] - Escherichia coli (strain O157:H7, subst  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: E90766  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Har gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 ar  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: E90766  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-91 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BAB34524.1; PID:g13360561; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECs1101

Query Match 100.0%; Score 20; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
||||  
Db 37 DLDA 40

## RESULT 36

F85716 unknown protein encoded within prophage CP-9330 [imported] - Escherichia coli (strain O157:H7)

C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: F85716  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F85716

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-91 <STO>

A:Cross-references: GB:AE005174; NID:gl2515079; PIDN:AAG56194.1; GSPDB:GN00145; UWGP:Z21

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z2124

## Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 91;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
||||  
Db 37 DLDA 40

## RESULT 37

E83305

hypothetical protein PA2723 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: E83305

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83305

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-92 <STO>

A:Cross-references: GB:AE004700; GB:AE004091; NID:g9948792; PIDN:AAG06111.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2723

## Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 92;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
||||  
Db 54 DLDA 67

## RESULT 38

agrocinopine phosphodiesterase [imported] - Agrobacterium tumefaciens (strain C58,

JC4564 antifungal protein precursor - Penicillium chrysogenum

C:Species: Penicillium chrysogenum

C:Date: 12-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jul-2000

C:Accession: JC4564

R:Marx, F.; Haas, H.; Reindl, M.; Stoeffler, G.; Lottspeich, F.; Redl, B.

Gene 167, 167-171, 1995

A:Title: Cloning, structural organization and regulation of expression of the Peni

A:Reference number: JC4564; MUID:96144269; PMID:8566771

A:Accession: JC4564

A:Molecule type: mRNA

A:Residues: 1-92 <MAR>

A:Cross-references: GB:U22944; NID:g862384; PIDN:AAA92718.1; PID:g862385

C:Comment: This protein is an abundantly secreted, highly basic, and cysteine-rich

C:Genetics:

A:Gene: paf

A:Introns: 42/3; 72/3

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-37/Domain: propeptide #status predicted <PRS>

F:38-92/Product: antifungal protein #status predicted <MAT>

Query Match 100.0%; Score 20; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
||||  
Db 27 DLDA 30

## RESULT 39

E83630

hypothetical protein PA0124 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: E83630

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: E83630

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-93 <STO>

A:Cross-references: GB:AE004450; GB:AE004091; NID:g9945943; PIDN:AAG03514.1; GSPDB

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0124

## Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 93;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DLDA 4  
||||  
Db 12 DLDA 15

## RESULT 40

AC3252

agrocinopine phosphodiesterase [imported] - Agrobacterium tumefaciens (strain C58,

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002

C:Accession: AC3252

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; M

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; M

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-K

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193  
A;Accession: AC3252  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-94 <KUR>  
A;Cross-references: GB:AE008690; PIDN:RAL  
A;Experimental source: strain C58 (Dupont  
C;Genetics:  
A;Gene: accf  
A;Genome: plasmid

```
Query Match      100.0%; Score 20; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4: Conservative 0; Mismatches 0; Indels
```

Qy 1 DLDA 4  
16 DLDA 19

RESULT 41

S3306 41  
S24146  
S-100 protein p - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Aug-1999  
C:Accession: S24146; PS0340  
R:Becker, T.; Gerke, V.; Kube, E.; Weber, K.  
Eur. J. Biochem. 207, 541-547, 1992  
A:Title: S100p, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recombinant

```
Query Match      100.0%; Score 20; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4: Conservative 0: Mismatches 0: Indels
```

QY	1	DLDA	4
Dh	60	DLDA	63

## RESULT 42

RESULT 4.2  
 S71519  
 M protein type 19 - Streptococcus pyogenes (fragment)  
 C:Species: Streptococcus pyogenes  
 C:Date: 06-dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
 C:Accession: S71519; S71515  
 R:Podbielski, A.; Melzer, B.; Lutticken, R.  
 submitted to the EMBL Data Library, November 1990  
 A:Description: Application of the polymerase chain reaction to study the M protein(-like  
 A:Reference number: S71518  
 A:Accession: S71519  
 A:Molecule type: DNA

A;Residues: 1-96 <POD>  
A;Cross-references: EMBL:X56609  
A;Experimental source: strain J17D/70  
R;Podbielski, A.; Melzer, B.; Lueticken, R.  
Med. Microbiol. Immunol. 180, 213-227, 1991  
A;Title: Application of the polymerase chain reaction to study the M protein(-like)  
A;Reference number: S71514; MUID:92149493; PMID:1784271  
A;Accession: S71515  
A;Molecule type: DNA  
A;Residues: 1-42 <POW>  
A;Cross-references: EMBL:X56609  
A;Experimental source: J17D/70  
C;Genetics:  
C;Gene: emm19  
C;Superfamily: M5 protein

Query Match 100.0%; Score 20; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 4: Conservative 0; Mismatches 0; Indels

QY	1	DLDA	4
Db	61	DLDA	64

## RESULT 43

H83065  
 hypothetical protein PA4542 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
 C:Species: *Pseudomonas aeruginosa*  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: H83065  
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.,  
 Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: H83065  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-96 \*STO>  
 A:Cross-references: GB:AE004878; GB:AE004091; NID:G9950888; PIDN:AGC08029.1; GSPDB  
 A:Experimental source: strain PA01  
 C:Genetics:  
 C:Gene: PA4542

```
Query Match      100.0%; Score 20; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	DLDA	4
Dh	62	DLDA	6

RESULT 44

RE5001\_44  
 H98254  
 hypothetical protein AGR\_L1980 [imported] - Agrobacterium tumefaciens (strain C58,  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 11-Jan-2002  
 C:Accession: H98254  
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Gol  
 A.; Liu, F.; Wollman, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markel  
 Science 294, 2323-2328, 2001  
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacteri  
 A:Reference number: A97359; PMID:11743194  
 A:Accession: H98254  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-97 <KUR>  
 A:Cross-references: GB:AE007870; PIDN:AAK89562.1; PID:gl5159447; GSPDB:GN00170  
 C:Genetics:  
 A:Gene(s): AGR\_L1980

A;Map position: linear chromosome

Query Match 100.0%; Score 20; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 45 DLDA 48

#### RESULT 45

S61079  
M protein precursor - Streptococcus pyogenes (serotype M19) (fragment)  
C;Species: Streptococcus pyogenes  
A;Variety: serotype M19  
C;Date: 15-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 16-Feb-1997  
C;Accession: S61079; S60799  
R;Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.  
submitted to the EMBL Data Library, July 1994  
A;Description: Noncongruent relationships between variation in emm1 gene sequences and t  
A;Reference number: S61072  
A;Accession: S61079  
A;Molecule type: DNA  
A;Residues: 1-98 <WHA>  
A;Cross-references: EMBL:U11959  
R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.  
Mol. Microbiol. 14, 619-631, 1994  
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop  
A;Reference number: S60784; MUID:95198537; PMID:7891551  
A;Accession: S60799  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 18-77 <WHW>  
A;Cross-references: EMBL:U11959  
C;Genetics:  
A;Gene: emm19  
C;Superfamily: M5 protein  
F;1-30/Domain: signal sequence (fragment) #status predicted <SIG>  
F;31-98/Product: M protein (fragment) #status predicted <MAP>

Query Match 100.0%; Score 20; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
|  
|  
|  
|  
Db 49 DLDA 52

Search completed: February 6, 2003, 11:23:04  
Job time : 12.5 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 5.33333 Seconds  
(without alignments)  
31.107 Million cell updates/sec

Title: PAT943-2  
Perfect score: 20  
Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 948

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	72	1 RL29_CHLPN	Q927f5 chlamydia p
2	20	100.0	74	1 ACP_STRPN	Q9fbc6 streptococc
3	20	100.0	74	1 ACP_STRPY	Q99yd3 streptococc
4	20	100.0	79	1 C551_ECTHL	P38587 ectothiorho
5	20	100.0	85	1 EX7S_MYCTU	O53455 mycobacteri
6	20	100.0	87	1 YSCF_YEREN	Q01247 yersinia en
7	20	100.0	91	1 S112_BOVIN	P79105 bos caurus
8	20	100.0	93	1 AAT_METEX	P52069 methylobact
9	20	100.0	95	1 S10P_HUMAN	P25815 homo sapien
10	20	100.0	98	1 S10Z_HUMAN	Q8wxg8 homo sapien
11	20	100.0	107	1 SSI_STRGI	P28592 streptomyc
12	20	100.0	110	1 GLPE_PSEAE	Q915u8 pseudomonas
13	20	100.0	112	1 AL17_ASFPU	O42799 aspergillus
14	20	100.0	113	1 GLNB_CYACA	Q9tm37 cyanidium c
15	20	100.0	116	1 CH15_DROVI	P13424 drosophila
16	20	100.0	120	1 VATF_HALN1	Q9hne2 halobacteri
17	20	100.0	122	1 YEPF_ECOLI	P33219 escherichia
18	20	100.0	123	1 RNPA_STRBI	P25817 streptomyc
19	20	100.0	123	1 RNPA_STRCO	P48206 streptomyc
20	20	100.0	124	1 VGI9_BPMD2	O64212 mycobacteri
21	20	100.0	129	1 CCDP_MAIZE	Q01595 zeamays (m
22	20	100.0	131	1 Y4TP_RHISN	P55499 rhizobium s
23	20	100.0	136	1 RNK_ECOLI	P40679 escherichia
24	20	100.0	137	1 INL2_DROME	Q9vt51 drosophila
25	20	100.0	140	1 ATPK_VIBCH	Q9knh6 vibrio chol
26	20	100.0	140	1 Y4UK_RHISN	P23205 pseudomonas
27	20	100.0	140	1 YK24_PSEAE	Q9k4f6 streptomyc
28	20	100.0	141	1 DTD_STRCO	Q9k4f6 streptomyc
29	20	100.0	141	1 HBA3_XENLA	P06636 xenopus lae
30	20	100.0	141	1 HBA3_XENTR	P08422 xenopus tro
31	20	100.0	142	1 MMS5_MYCTU	O53785 mycobacteri
32	20	100.0	144	1 RL11_STRAT	Q87085 streptomyc
33	20	100.0	144	1 RL11_STRGR	P36258 streptomyc

34	20	100.0	144	1 RL11_STRSQ	Q07975 streptomyc
35	20	100.0	146	1 RBFA_RHILO	Q98b17 rhizobium l
36	20	100.0	152	1 GLBP_CHITH	P11582 chironomus
37	20	100.0	152	1 RS15_ATH	Q08112 arabidopsis
38	20	100.0	152	1 RS15_PODAN	P34737 podospora a
39	20	100.0	154	1 Y194_AQUAE	O65575 aquifex aeo
40	20	100.0	155	1 DUT_CAUCR	Q9a253 caulobacter
41	20	100.0	156	1 YS51_MYCTU	O05808 mycobacteri
42	20	100.0	157	1 YE19_MYCTU	P71688 mycobacteri
43	20	100.0	158	1 ATPX_SYNCP6	P08446 synecococc
44	20	100.0	163	1 ATPX_ANASP	P12410 anabaena sp
45	20	100.0	168	1 FUSE_BURCE	P24130 burkholderi

## ALIGNMENTS

RESULT 1  
ID RL29\_CHLPN STANDARD; PRT; 72 AA.  
AC Q927f5: Q9JQG5;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 50S ribosomal protein L29.  
GN RPMC OR RL29 OR CPN0639 OR CP0108.  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CWL029;  
RX MEDLINE=99206606; PubMed=10192388;  
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia  
RT pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CW029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
CC -1- SIMILARITY: BELONGS TO THE L29P FAMILY OF RIBOSOMAL PROTEINS.  
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CC  
DR EMBL: AE001647; RAD18778.1; -;  
DR EMBL: AF002173; AAF37991.1; -;  
DR EMBL: AF002547; BAA98846.1; -;  
DR TIGR: CP0108; -;  
DR InterPro: IPR001854; Ribosomal\_L29.

DR PROSITE; PS00579; RIBOSOMAL\_L29; FALSE\_NEG.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 72 AA; 8197 MW; 1C7E974B83C852C2 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 72;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 18 DLDA 21

## RESULT 2

ID	ACP_STRPN	STANDARD;	PRT;	74 AA.
AC	Q9FBC6;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Acyl carrier protein (ACP).			
GN	ACPP OR SP0418.			
OS	Streptococcus pneumoniae.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1313;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=R6;			
RC	MEDLINE=20365714; PubMed=10910344;			
RT	Heath R.J., Rock C.O.;			
RT	"A triclosan-resistant bacterial enzyme.";			
PL	Nature 406:145-146(2000).			
[2]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TIGR4;			
RC	MEDLINE=21357209; PubMed=11463916;			
RA	Tetelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,			
RA	Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,			
RA	Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,			
RA	Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,			
RA	Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,			
RA	McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,			
RA	Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,			
RA	Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;			
RT	"Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";			
RL	Science 293:498-506(2001).			
CC	-!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).			
CC	-!- PATHWAY: De novo fatty acid biosynthesis.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphydryl of the prosthetic group (By similarity).			
CC	-!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.			
CC				
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CC				
DR	EMBL; AF197933; AAF98272.1; -;			
DR	EMBL; AE007353; AAK74581.1; -;			
DR	HSSP; P02901; 1ACP.			
DR	TIGR; SP0418; -;			
DR	InterPro; IPR003231; Acyl_carrier.			
DR	InterPro; IPR003880; Ppantne_attach.			
DR	Pfam; PF00550; pp-binding; 1.			

DR ProDom; PD000887; Acyl\_carrier; 1.  
DR PROSITE; PS00075; ACP\_DOMAIN; 1.  
DR PROSITE; PS00112; PHOSPHOPANTHETHEINE; FALSE\_NEG.  
KW Lipid synthesis; Fatty acid biosynthesis; Phosphopantetheine;  
KW Complete proteome. 35 PHOSPHOPANTHETHEINE (BY SIMILARITY).  
FT BINDING 35  
SQ SEQUENCE 74 AA; 8268 MW; E2E9A78567090C14 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 74;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|||||  
Db 30 DLDA 33

## RESULT 3

ID	ACP_STRPY	STANDARD;	PRT;	74 AA.
AC	Q99YD3;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Acyl carrier protein (ACP).			
GN	ACPP OR SPY1753 OR SPYM18_1825.			
OS	Streptococcus pyogenes, and			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314, 186103;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;			
RC	MEDLINE=21192684; PubMed=11296296;			
RA	Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
RA	Xuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
[2]				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MGAS8232 / Serotype M18;			
RC	MEDLINE=21927593; PubMed=11917108;			
RA	Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,			
RA	Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,			
RA	Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,			
RA	Kapur V., Daly J.A., Veasy L.G., Musser J.M.;			
RT	"Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
CC	-!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis (By similarity).			
CC	-!- PATHWAY: De novo fatty acid biosynthesis.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).			
CC	-!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphydryl of the prosthetic group (By similarity).			
CC	-!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.			
CC				
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CC				
DR	EMBL; AE006603; AAK34496.1; -;			
DR	EMBL; AE010089; AAL98344.1; -;			



```

DR HSSP; P02901; IACP.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Peptide_attach.
DR Pfam; PF00550; pp-binding; 1.
DR ProDom; PD000887; Acyl_DOMAIN; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; FALSE_NEG.
KW Lipid synthesis; Fatty acid biosynthesis; Phosphopantetheine;
KW Complete proteome.
FT BINDING 35 35 PHOSPHOPANTHETHEINE (BY SIMILARITY).
SQ SEQUENCE 74 AA; 8343 MW; 41D7F77F23065B44 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 4
C551_ECTHL
ID C551_ECTHL STANDARD; PRT; 79 AA.
AC P38587;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c-551 (C551).
OS Ectothiorhodospira halochloris.
OC Bacteria; Proteobacteria; gamma subdivision; Ectothiorhodospiraceae;
OC Halorhodospira.
OX NCBI_TaxID=1052;
RN [1]
RP SEQUENCE.
RA MEDLINE=94028993; PubMed=8215425;
RA Ambler R.P., Meyer T.E., Kamen M.D.;
RT "Amino acid sequences of cytochromes c-551 from the halophilic purple
RT phototrophic bacteria, Ectothiorhodospira halophila and E.
RT halochloris."
RL Arch. Biochem. Biophys. 306:83-93(1993).
CC -1- MISCELLANEOUS: ECTOTHIORHODOSPIRA IS A GENUS OF PURPLE, SULFUR,
CC PHOTOSYNTHETIC BACTERIA THAT DEPOSIT SULFUR GLOBULES OUTSIDE THEIR
CC CELLS.
DR PIR; S38756; S38756.
DR HSSP; P00122; 1GKS.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; CytC_C1.
DR Pfam; PF00034; cytochrome_c; 1.
DR PRINTS; PR00607; CYTOCHROME_CIE.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme.
FT BINDING 14 14 HEME (COVALENT).
FT BINDING 17 17 HEME (COVALENT).
FT METAL 18 18 IRON (HEME AXIAL LIGAND).
FT METAL 55 55 IRON (HEME AXIAL LIGAND).
SQ SEQUENCE 79 AA; 8355 MW; EA6CEA2EF2BA5995 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 38 DLDA 41

RESULT 5
EX7S_MYCTU
ID EX7S_MYCTU STANDARD; PRT; 85 AA.
AC O53455;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
DE (Exonuclease VII small subunit).
GN XSEB OR RV1107C OR MT1138 OR MTV017.60C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RC Peterson J., DeBoy R., Dodson R., Gwinn M.B., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BIDIRECTIONALLY DEGRADES SINGLE-STRANDED DNA INTO LARGE
CC ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER
CC INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' to 3'
CC or 3' to 5' direction to yield nucleoside 5'-phosphates.
CC -1- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE XSEB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL021897; CAAL7223.1; -.
DR EMBL; AE006993; AAK45395.1; ALT_INIT.
DR TIGR; MT1138; -.
DR Tuberculist; RV1107c; -.
DR InterPro; IPR003761; Exonuc_VII_S.
DR Pfam; PF02609; Exonuc_VII_S; 1.
DR TIGRFAMs; TIGR01280; xseB; 1.
DR TIGRFAHs; Nuclease; Exonuclease; Complete proteome.
KW Hydrolyase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 85 AA; 9322 MW; ACD4756808DA79A8 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 44 DLDA 47

RESULT 6

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YSCF\_YEREN  
ID YSCF\_YEREN STANDARD; PRT; 87 AA.  
AC Q01247;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE YOP proteins translocation protein F.  
GN YSCF  
OS Yersinia enterocolitica.  
OG Plasmid pIV.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Yersinia.  
OX NCBI\_TaxID=630;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-439-80 / Serotype O:9;  
RA MEDLINE=913171716; PubMed=1860816;  
RX Michiels T., Vancotteghem J.-C., de Rouvroit C., China B., Gustin A.,  
RA Boudry P., Cornelis G.R.;  
RT "Analysis of virC, an operon involved in the secretion of Yop  
proteins by Yersinia enterocolitica.";  
RL J. Bacteriol. 173:4994-5009(1991).  
CC -1- INDUCTION: AT 37 DEGREES CELSIUS IN THE ABSENCE OF CALCIUM.  
CC -1- MISCELLANEOUS: BELONGS TO AN OPERON INVOLVED IN THE TRANSLOCATION  
OF YOP PROTEINS ACROSS THE BACTERIAL MEMBRANES OR IN THE SPECIFIC  
CONTROL OF THIS FUNCTION.  
CC -1- SIMILARITY: BELONGS TO THE MXTH/PRGI/YSCF FAMILY.  
CC  
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CC  
CC EMBL; M74011; AAC37023.1; -;  
DR PIR; F40361.  
KW Virulence; Plasmid; Transport; Protein transport.  
SQ SEQUENCE 87 AA; 9449 MW; 90E78542BB267CF6 CRC64;  
  
Query Match 100.0%; Score 20; DB 1; Length 87;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
DB 15 DLDA 18  
  
RESULT 7  
S112\_BOVIN  
ID S112\_BOVIN STANDARD; PRT; 91 AA.  
AC P79105;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Calgranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)  
DE (CAAF1) (RAGE binding protein).  
GN S100A12 OR CAAF1.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Oesophagus;  
RX MEDLINE=96298783; PubMed=8718672;  
RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,  
RA Nagasaki K.;  
RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its  
molecular cloning and tissue distribution.";

J. Cell Sci. 109:805-815(1996).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=99325504; PubMed=10399917;  
RA Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C.,  
RA Kambham N., Bierhaus A., Nawroth P., Neurath M.F., Slattery T.,  
RA Beach D., McClary J., Nagashima M., Morser J., Stern D.,  
RA Schmidt A.M.;  
RT "RAGE mediates a novel proinflammatory axis: a central cell surface  
receptor for S100/calgranulin polypeptides.";  
RL Cell 97:889-901(1999).  
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
CC  
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CC  
CC EMBL; D49548; BAA08496.1; -;  
DR EMBL; AF011757; AAB65423.1; -;  
DR HSSP; P80511; 1E8A.  
DR InterPro; IPR001751; CAbP\_S100.  
DR InterPro; IPR002048; EF-hand.  
DR Pfam; PF00036; ehand; 1.  
DR Pfam; PF01023; S\_100; 1.  
DR ProDom; PD000012; EF-hand; 1.  
DR ProDom; PD003407; CAbP\_S100; 1.  
DR PROSITE; PS00018; EF\_HAND; 1.  
DR PROSITE; PS00303; S100\_CABP; 1.  
KW Calcium-binding; zinc; Metal-binding.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT CA\_BIND 18 31 EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).  
FT CA\_BIND 61 72 EF-HAND 2 (HIGH AFFINITY) (BY  
SIMILARITY).  
FT SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;  
  
Query Match 100.0%; Score 20; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.7e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
DB 59 DLDA 62  
  
RESULT 8  
AAT\_METEX  
ID AAT\_METEX STANDARD; PRT; 93 AA.  
AC P52069;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Putative aspartate aminotransferase (EC 2.6.1.1) (Transaminase A)  
DE (ASPA) (ORF2) (Fragment).  
OS Methylobacterium extorquens.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Methylobacterium group; Methylobacterium.  
OX NCBI\_TaxID=408;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IBT 6;  
RX MEDLINE=93305286; PubMed=7763712;  
RA Valentin H.E., Steinbuechel A.;  
RT "Cloning and characterization of the Methylobacterium extorquens  
polyhydroxyalkanoic-acid-synthase structural gene.";  
RL Appl. Microbiol. Biotechnol. 39:309-317(1993).  
CC -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
L-glutamate.

CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).  
 CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC -----  
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 CC -----  
 CC EMBL; L07893; AAA72329.1; -.  
 CC HSSP; Q5G232; IBLW.  
 CC InterPro; IPR004838; NHtransf\_1.  
 CC PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; PARTIAL.  
 CC Hypothetical protein; Transferase; Aminotransferase;  
 CC Pyridoxal phosphate. 93  
 CC NON\_TER 93  
 CC SEQUENCE 93 AA; 10424 MW; 201376961C632611 CRC64;  
 CC -----  
 CC Query Match 100.0%; Score 20; DB 1; Length 93;  
 CC Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Qy 1 DLDA 4  
 CC Db 41 DLDA 44  
 CC -----  
 CC RESULT 9  
 CC S10P\_HUMAN  
 CC ID S10P\_HUMAN STANDARD; PRT; 95 AA.  
 CC AC P25815;  
 CC DT 01-MAY-1992 (Rel. 22, Created)  
 CC DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE S-100P protein.  
 CC GN S100P OR S100E.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Placenta;  
 CC RX MEDLINE=92339442; PubMed=1633809;  
 CC RA Becker T., Gerke V., Kube E., Weber K.;  
 CC RT "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA  
 CC cloning, recombinant protein expression and Ca2+ binding  
 CC properties.";  
 CC RL Eur. J. Biochem. 207:541-547(1992).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Placenta;  
 CC RA Strausberg R.;  
 CC RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC RN [3]  
 CC RP SEQUENCE OF 1-91.  
 CC RC TISSUE=Placenta;  
 CC RX MEDLINE=92171935; PubMed=1540168;  
 CC RA Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;  
 CC RT "Purification and characterization of a new member of the S-100  
 CC protein family from human placenta.";  
 CC RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).  
 CC CC -|- SUBUNIT: Interacts with S100Z.  
 CC CC -|- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.  
 CC CC -|- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
 CC -----  
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 CC -----  
 CC EMBL; X65614; CAA46566.1; -.  
 CC EMBL; BC006819; AAH06819.1; -.  
 CC PIR; S24146; S24146.  
 CC HSSP; P02638; 1CFP.  
 CC Genew; HGNC:10504; S100P.  
 CC MIM; 600614; -.  
 CC InterPro; IPR001751; CaBP\_S100.  
 CC InterPro; IPR002048; EF-hand.  
 CC Pfam; PF00036; efhand; 1.  
 CC Pfam; PF01023; S100; 1.  
 CC ProDom; PD003407; CaBP\_S100; 1.  
 CC PROSITE; PS00018; EF\_HAND; FALSE\_NEG.  
 CC PROSITE; PS00303; S100\_CABP; 1.  
 CC KW Calcium-binding; Placenta.  
 CC FT CA\_BIND 19 32 EF-HAND 1 (LOW AFFINITY).  
 CC FT CA\_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).  
 CC FT CONFLICT 32 32 E -> T (IN REF. 3).  
 CC FT CONFLICT 44 44 F -> E (IN REF. 3).  
 CC SQ SEQUENCE 95 AA; 10400 MW; 786E6E3F3EACC6C1 CRC64;  
 CC -----  
 CC Query Match 100.0%; Score 20; DB 1; Length 95;  
 CC Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC -----  
 CC Qy 1 DLDA 4  
 CC Db 60 DLDA 63  
 CC -----  
 CC RESULT 10  
 CC S10Z\_HUMAN  
 CC ID S10Z\_HUMAN STANDARD; PRT; 98 AA.  
 CC AC Q8WXG8;  
 CC DT 15-JUN-2002 (Rel. 41, Created)  
 CC DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 CC DE S-100Z protein.  
 CC GN S100Z.  
 CC OS Homo sapiens (Human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 CC OX NCBI\_TaxID=9606;  
 CC RN [1]  
 CC RP SEQUENCE FROM N.A.; SEQUENCE OF 1-20, SUBUNIT, CALCIUM-BINDING,  
 CC TISSUE SPECIFICITY, AND INTERACTION WITH S100P.  
 CC RC TISSUE=Prostate;  
 CC RX MEDLINE=21614385; PubMed=11747429;  
 CC RA Gribenko A.V., Hopper J.E., Makhatadze G.I.;  
 CC RT "Molecular characterization and tissue distribution of a novel member  
 CC of the S100 family of EF-hand proteins.";  
 CC RL Biochemistry 40:15538-15548(2001).  
 CC RN [2]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Testis;  
 CC RA Strausberg R.;  
 CC RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 CC CC -|- SUBUNIT: Homodimer. Interacts with S100P.  
 CC CC -|- TISSUE SPECIFICITY: Highest level of expression in spleen and  
 CC leukocytes.  
 CC CC -|- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.  
 CC CC -|- SIMILARITY: BELONGS TO THE S-100 FAMILY.  
 CC CC -|- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.  
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CC -----  
CC EMBL; AF437876; AAL30893.1; -  
CC EMBL; BC022320; AAH22320.1; -  
CC InterPro; IPR001751; CaBP\_S100.  
CC InterPro; IPR002048; EF-hand.  
CC Pfam; PF00036; efhand; 1.  
CC PROSITE; PS001023; S\_100; 1.  
CC PROSITE; PS00018; EF\_HAND; 1.  
CC Calcium-binding.  
CC INIT\_MET 0  
CC CA\_BIND 19 32 EF-HAND 1 (LOW AFFINITY).  
CC CA\_BIND 62 73 EF-HAND 2 (HIGH AFFINITY).  
CC SEQUENCE 98 AA; 11430 MW; A2053E1809F0F401 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4  
| | | |  
Db 60 DLDA 63

RESULT 11  
SSI\_STRGI STANDARD; PRT; 107 AA.  
AC P28592;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Alkaline protease inhibitor 2C' (API-2C').  
OS Streptomyces griseolincarnatus.  
CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
CC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=29305;  
RN [1]  
RP SEQUENCE.  
RA Suzuki K., Uyeda M., Shibata M.;  
RT "Partial amino acid sequence of an alkaline protease inhibitor, API-2 (b and c).";  
RL Agric. Biol. Chem. 45:629-634(1981).  
CC -!- FUNCTION: STRONG INHIBITORY ACTIVITY TOWARD SUBTILISIN.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE SERINE PROTEASE INHIBITORS SSI FAMILY.  
CC HSP; P01006; 2SIC.  
DR InterPro; IPR000691; strep\_subt\_inhib.  
DR Pfam; PF00720; SSI; 1.  
DR PRINTS; PR00294; SSBTLINHBT.  
DR ProDom; PD004028; Strep\_subt\_inhib; 1.  
DR PROSITE; PS00999; SSI; 1.  
KW Serine protease inhibitor.  
FT DISULFID 29 44 BY SIMILARITY.  
FT DISULFID 65 95 BY SIMILARITY.  
FT ACT\_SITE 67 68 REACTIVE BOND.  
SQ SEQUENCE 107 AA; 10972 MW; 76043BA9F876D1CA CRC64;

Query Match 100.0%; Score 20; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4  
| | | |  
Db 53 DLDA 56

RESULT 12  
GLPE\_PSEAE STANDARD; PRT; 110 AA.  
ID GLPE\_PSEAE  
AC Q915U8;  
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DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Thiosulfate sulfitransferase glpE (EC 2.8.1.1).  
GN GLPE OR PA0589.  
OS Pseudomonas aeruginosa.  
CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
CC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RC MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
CC -!- FUNCTION: Catalyzes, although with low efficiency, the sulfur transfer reaction from thiosulfate to cyanide (By similarity).  
CC -!- CATALYTIC ACTIVITY: Thiosulfate + cyanide -> sulfite + thiocyanate.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE GLPE FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.  
CC -----  
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CC -----  
CC EMBL; AE004495; AAG03978.1; -  
CC InterPro; IPR001763; Rhodanese-like.  
DR Pfam; PF00581; Rhodanese; 1.  
DR SMART; SM00450; RHOD; 1.  
KW Transferase; Glycerol metabolism; Complete proteome.  
FT ACT\_SITE 65 65 BY SIMILARITY.  
SQ SEQUENCE 110 AA; 11963 MW; B0C009A0FDDFD1FC CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 110;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 DLDA 4  
| | | |  
Db 56 DLDA 59

RESULT 13  
ALL7 ASPFU STANDARD; PRT; 112 AA.  
ID ALL7 ASPFU  
AC O42799;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Allergen Asp f 7 (Fragment).  
OS Aspergillus fumigatus (Sartorya fumigata).  
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
CC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5085;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 4202 / AF-102;  
RC MEDLINE=98141802; PubMed=9482698;  
RA Cramer R.;  
RT "Recombinant Aspergillus fumigatus allergens: from the nucleotide sequences to clinical applications.";

RL Int. Arch. Allergy Immunol. 115:99-114(1998).  
-----  
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-----  
DR EMBL: AJ223315; CAA11255.1; -  
KW Allergen.  
FT NON\_TER 1 1  
SQ SEQUENCE 112 AA; 11628 MW; EF64A9B2D4844F6F CRC64;  
  
Query Match 100.0%; Score 20; DB 1; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DLDA 4  
Db 85 DLDA 88  
  
RESULT 14  
ID GLNB\_CVACA STANDARD; PRT; 113 AA.  
AC Q9TM37;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Nitrogen regulatory protein P-II.  
GN GLNB.  
OS Cyanidium caldarium.  
OG Chloroplast.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;  
OC Cyanidium.  
CC NCBI\_TaxID=2771;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20496959; PubMed=11040290;  
RT Gloeckner G., Rosenthal A., Valentin K.-U.;  
RT "The structure and gene repertoire of an ancient red algal plastid  
genome.";  
RL J. Mol. Evol. 51:382-390(2000).  
CC -!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE  
CC GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED  
CC CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL  
CC ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE  
CC EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE  
CC DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE  
CC DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE P(II) PROTEIN FAMILY.  
-----  
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-----  
DR EMBL: AF022186; AAF13016.1; -  
DR HSSP: P05826; 2PII.  
DR InterPro: IPR002332; PII\_GlnB\_UMP.  
DR InterPro: IPR002187; PII\_glnb.  
DR Pfam: PF00543; P-II; 1.  
DR PRINTS: PR00340; PIIglnb.  
DR ProDom: PD001194; PII\_glnB; 1.  
DR PROSITE: PS00496; PII\_GlnB\_UMP; FALSE\_NEG.

DR PROSITE: PS00638; PII\_GlnB\_CTER; 1.  
KW Transcription regulation; Nitrogen fixation; Chloroplast.  
FT BINDING 52 52 UMP (BY SIMILARITY).  
SQ SEQUENCE 113 AA; 12602 MW; 83C9468B2A3C83BC CRC64;  
  
Query Match 100.0%; Score 20; DB 1; Length 113;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DLDA 4  
Db 109 DLDA 112  
  
RESULT 15  
CH15\_DROVI STANDARD; PRT; 116 AA.  
AC PI3424;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Chorion protein S15.  
GN CP15 OR S15.  
OS Drosophila virilis (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88297142; PubMed=3136055;  
RA Martinez-Cruzado J.C., Swimmer C., Fenerjian M.G., Kafatos F.C.;  
RT "Evolution of the autosomal chorion locus in Drosophila. I. General  
RT organization of the locus and sequence comparisons of genes s15 and  
RT s19 in evolutionary distant species.";  
RL Genetics 119:663-677(1988).  
-----  
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-----  
DR EMBL: X53421; CAA37501.1; -  
DR FIR; S06614; S06614.  
DR FlyBase: FBgn0013068; Dvir\Cpl5.  
KW Chorion.  
SQ SEQUENCE 116 AA; 11990 MW; 8FB7E77C87E75777 CRC64;  
  
Query Match 100.0%; Score 20; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DLDA 4  
Db 98 DLDA 101  
  
RESULT 16  
VATF\_HALNI STANDARD; PRT; 120 AA.  
AC Q9HNE2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE V-type ATP synthase subunit F (EC 3.6.3.14) (V-type ATPase subunit F).  
GN ATPF OR VNG2140G.  
OS Halobacterium sp. (strain NRC-1).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;

RN SEQUENCE FROM N.A.  
 RX MEDLINE=20504483; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
 RA Leithaus B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;  
 RT "Genome sequence of Halobacterium species NRC-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
 CC GRADIENT ACROSS THE MEMBRANE.  
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +  
 CC H(+)(Out).  
 CC -!- SIMILARITY: BELONGS TO THE V-ATPASE F SUBUNIT FAMILY.  
 CC  
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 CC -----  
 DR EMBL; AE005102; AAG20278.1; -;  
 DR InterPro; IPR002841; ATPsynt\_Fsub.  
 DR Pfam; PF01990; ATP-synt\_F; 1.  
 DR ProDom; PD003811; ATPsynt\_Fsub; 1.  
 DR Hydrolase; ATP synthesis; Hydrogen ion transport; Complete proteome.  
 KW SEQUENCE 120 AA; 12388 MW; 9A88D7D7FF21631 CRC64;  
 SQ  
 Query Match 100.0%; Score 20; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 Db 36 DLDA 39  
 RESULT 17  
 YEBF\_ECOLI  
 ID YEBF\_ECOLI STANDARD; PRT; 122 AA.  
 AC P33219;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical lipoprotein yebf precursor.  
 GN YEBF OR B1847.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX Smith J.M., Nygaard P.;  
 RA Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 [3]  
 RN SEQUENCE FROM N.A.

RC STRAIN-K12;  
 RX MEDLINE=97251358; PubMed=9097040;  
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,  
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,  
 RA Saito N., Sempel G., Seki Y., Sivasubraman S., Tagami H.,  
 RA Takeda J., Takenoto K., Wada C., Yamamoto Y., Horiuchi T.;  
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
 RL corresponding to the 40.1-50.0 min region on the linkage map.";  
 RL DNA Res. 3:379-392(1996).  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
 CC (potential).  
 CC -----  
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 CC -----  
 DR EMBL; L20897; AAA23859.1; -;  
 DR EMBL; AE000278; AAC74917.1; -;  
 DR EMBL; D90827; BAA15653.1; -;  
 DR Ecogene; Egl1807; yebF.  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Hypothetical protein; Membrane; Lipoprotein; Signal;  
 KW Complete proteome.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 122 HYPOTHETICAL LIPOPROTEIN YEBF.  
 FT LIPID 20 20 N-ACYL DIGLYCERIDE (POTENTIAL).  
 FT SEQUENCE 122 AA; 13464 MW; EC941612C666BE88 CRC64;  
 SQ  
 Query Match 100.0%; Score 20; DB 1; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DLDA 4  
 Db 41 DLDA 44  
 RESULT 18  
 RNPA\_STRBI  
 ID RNPA\_STRBI STANDARD; PRT; 123 AA.  
 AC P25817;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase  
 DE P protein) (protein C5).  
 GN RNPA.  
 OS Streptomyces bikiniensis.  
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
 OC Actinomycetales; Streptomyceineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1896;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-Var. Zorbonensis;  
 RX MEDLINE=92354937; PubMed=1379566;  
 RM Morse D.P., Schmidt F.J.;  
 RT "Sequences encoding the protein and RNA components of ribonuclease P  
 RL from Streptomyces bikiniensis var. zorbonensis.";  
 RL Gene 117:61-66(1992).  
 CC -!- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence  
 CC from pre-tRNA to produce the mature 5' terminus. It can also  
 CC cleave other RNA substrates such as 4.5S RNA. The protein  
 CC component plays an auxiliary but essential role in vivo by binding  
 CC to the 5'-leader sequence and broadening the substrate specificity  
 CC of the ribozyme.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-  
 CC extra-nucleotide from tRNA precursor.

```

CC  -!- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC  protein subunit.
CC  -!- SIMILARITY: BELONGS TO THE RNPA FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; M83112; AAA26808.1; -
CC  PIR; JG1202; JC1202.
CC  InterPro; IPR00100; Ribonuclease_P.
CC  Pfam; PF00825; Ribonuclease_P; 1.
CC  TIGRFAMs; TIGR00188; rnpA; 1.
CC  PROSITE; PS00648; RIBONUCLEASE_P; 1.
CC  HydroLase; Nuclease; Endonuclease; tRNA processing; RNA-binding.
CC  KW  SEQUENCE 123 AA; 13145 MW; F89F595E046F33FC CRC64;
CC  -----
CC  Query Match 100.0%; Score 20; DB 1; Length 123;
CC  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
CC  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  -----
CC  QY 1 DLDA 4
CC  Db 109 DLDA 112
CC  ||||
CC  -----
CC  RESULT 19
CC  RNPA_STRCO
CC  ID RNPA_STRCO STANDARD; PRT; 123 AA.
CC  AC P48206;
CC  DT 01-FEB-1996 (Rel. 33, Created)
CC  DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC  DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC  DE Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
CC  DE P protein) (Protein C5).
CC  GN RNPA OR SCO3881 OR STE24.03.
CC  OS Streptomyces coelicolor.
CC  OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
CC  OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
CC  OX NCBI_TaxID=1902;
CC  RN [1]
CC  RP SEQUENCE FROM N.A.
CC  RC STRAIN-A3(2);
CC  RX MEDLINE=92250416; PubMed=1577691;
CC  RA Calcutt M.J., Schmidt F.J.;
CC  RT "Conserved gene arrangement in the origin region of the Streptomyces
CC  RT coelicolor chromosome."
CC  RL J. Bacteriol. 174:3220-3226(1992).
CC  RN [2]
CC  RP SEQUENCE FROM N.A.
CC  RC STRAIN-A3(2) / M145;
CC  RX MEDLINE=21996410; PubMed=12000953;
CC  RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.M., Challis G.L.,
CC  RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
CC  RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
CC  RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
CC  RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
CC  RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
CC  RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
CC  RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
CC  RA Hopwood D.A.;
CC  RT "Complete genome sequence of the model actinomycete Streptomyces
CC  RT coelicolor A3(2).";
CC  RL Nature 417:141-147(2002).
CC  -!- FUNCTION: RNaseP catalyzes the removal of the 5'-leader sequence
CC  from pre-tRNA to produce the mature 5' terminus. It can also
CC  cleave other RNA substrates such as 4.5S RNA. The protein
CC  component plays an auxiliary but essential role in vivo by binding
CC  to the 5'-leader sequence and broadening the substrate specificity

```

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CC  of the ribozyme (By similarity).
CC  -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC  extra-nucleotide from tRNA precursor.
CC  -!- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC  protein subunit (By similarity).
CC  -!- SIMILARITY: BELONGS TO THE RNPA FAMILY.
CC  -----
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CC  -----
CC  EMBL; AF187159; AAA26732.1; -
CC  EMBL; AL049826; CAB42696.1; -
CC  InterPro; IPR00100; Ribonuclease_P.
CC  Pfam; PF00825; Ribonuclease_P; 1.
CC  TIGRFAMs; TIGR00188; rnpA; 1.
CC  PROSITE; PS00648; RIBONUCLEASE_P; 1.
CC  HydroLase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
CC  KW  Complete proteome.
CC  SQ SEQUENCE 123 AA; 13320 MW; 0D4D4E26A20B6C39 CRC64;
CC  -----
CC  Query Match 100.0%; Score 20; DB 1; Length 123;
CC  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
CC  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  -----
CC  QY 1 DLDA 4
CC  Db 109 DLDA 112
CC  ||||
CC  -----
CC  RESULT 20
CC  VG19_BPMD2
CC  ID VG19_BPMD2 STANDARD; PRT; 124 AA.
CC  AC O64212;
CC  DT 15-DEC-1998 (Rel. 37, Created)
CC  DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC  DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC  DE Gene 19 protein (gp19).
CC  GN 19.
CC  OS Mycobacteriophage D29.
CC  OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
CC  OC unclassified Siphoviridae.
CC  OX NCBI_TaxID=28369;
CC  RN [1]
CC  RP SEQUENCE FROM N.A.
CC  RX MEDLINE=98300335; PubMed=9636706;
CC  RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
CC  RT "Genome structure of mycobacteriophage D29: implications for phage
CC  RT evolution."
CC  RL J. Mol. Biol. 279:143-164(1998).
CC  -----
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CC  -----
CC  EMBL; AF022214; AAC18459.1; -
CC  SQ SEQUENCE 124 AA; 14135 MW; F85A03C16A742837 CRC64;
CC  -----
CC  Query Match 100.0%; Score 20; DB 1; Length 124;
CC  Best Local Similarity 100.0%; Pred. No. 2.3e+02;
CC  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC  -----
CC  QY 1 DLDA 4
CC  Db 42 DLDA 45
CC  ||||
CC  -----

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## RESULT 21

CCDP\_MAIZE STANDARD; PRT; 129 AA.  
AC Q01595;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE Cortical cell delineating protein precursor (Root-specific protein ZRP3).  
DE ZRP3).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;  
OC Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A. TISSUE=Root;  
RC STRAIN=CV. NKH31; TISSUE=Root;  
RX MEDLINE=9309234; PubMed=1463822;  
RA John I., Wang H., Held B.M., Wurtele E.S., Colbert J.T.;  
RT "An mRNA that specifically accumulates in maize roots delineates a novel subset of developing cortical cells.";  
RL Plant Mol. Biol. 20:821-831(1992).  
CC -!- FUNCTION: DELINEATES A NOVEL SUBSET OF DEVELOPING CORTICAL CELLS. IT IS PROBABLY INVOLVED IN SOME ASPECT OF TRANSPORT OF MOLECULES TO OR FROM THE VASCULATURE.  
CC -!- TISSUE SPECIFICITY: CORTICAL GROUND MERISTEM OF DEVELOPING ROOTS.  
CC -!- SIMILARITY: STRONG; TO CARROT DC2.15 AND PEMB3.  
CC -----  
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CC -----  
DR EMBL; Z12103; CAA78088.1; -;  
DR PIR; S28009; S28009.  
DR HSSP; P24337; LHP.  
DR MaizeDB; 65581; -;  
DR InterPro; IPR003612; AAI.  
DR InterPro; IPR001768; Try/amy1\_inhptr.  
DR Pfam; PF00234; try\_alpha\_amy1; 1.  
DR SMART; SM00499; AAI; 1.  
DR Signal; Glycoprotein; Repeat.  
FT SIGNAL 1 19 OR 21 (POTENTIAL).  
FT CHAIN 20 129 CORTICAL CELL DELINEATING PROTEIN.  
FT CARBOHYD 25 25 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DOMAIN 29 40 2 X 6 AA TANDEM REPEATS OF P-V-V-P-T-P.  
FT REPEAT 29 34 1.  
FT REPEAT 35 40 2.  
SQ SEQUENCE 129 AA; 13526 MW; 39AAE618761D948B CRC64;

Query Match 100.0%; Score 20; DB 1; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 84 DLDA 87

## RESULT 22

Y4IP\_RHISN STANDARD; PRT; 131 AA.  
ID Y4IP\_RHISN  
AC P55499;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Hypothetical 14.4 kDa protein Y4IP.  
GN Y4IP.  
OS Rhizobium sp. (strain NGR234).  
OG Plasmid sym pNGR234a.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97305956; PubMed=9163424;  
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.;  
RT "Molecular basis of symbiosis between Rhizobium and legumes.";  
RL Nature 387:394-401(1997).  
CC -!- SIMILARITY: NONE OBVIOUS EXCEPT FOR SIMILARITY TO N-TERMINAL OF PUTATIVE TRANSPOSASE Y4RK. POTENTIAL FRAGMENT.  
CC -----  
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CC -----  
DR EMBL; AE000079; AAB91711.1; -;  
DR Hypothetical protein; Plasmid.  
SQ SEQUENCE 131 AA; 14387 MW; 9F2AE3B1FC6EC6CF CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 131;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
Db 15 DLDA 18

## RESULT 23

RNK\_ECOLI STANDARD; PRT; 136 AA.  
ID RNK\_ECOLI  
AC P40679;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Regulator of nucleoside diphosphate kinase.  
GN RNK OR B0610 OR Z0754 OR ECS0649.  
OS Escherichia coli, and  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562, 83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96015444; PubMed=7565093;  
RA Schlichtman D., Shankar S., Chakrabarty A.M.;  
RT "The Escherichia coli genes ssrA and rnk can functionally replace the Pseudomonas aeruginosa alginate regulatory gene algR2.";  
RL Mol. Microbiol. 16:309-320(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;  
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.



104  
RC SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Ikemoto K., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Oshima T., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
[5]  
RC SEQUENCE FROM N.A.  
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;  
RX MEDLINE=21074935; PubMed=11206551;  
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouisis K.,  
RA Prodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
RA Welch R.A., Blattner F.R.;  
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
RL Nature 409:529-533(2001).  
[6]  
RC SEQUENCE FROM N.A.  
RC STRAIN-O157:H7 / RMD 0509952;  
RX MEDLINE=21152331; PubMed=11258796;  
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
RT O157:H7 and genomic comparison with a laboratory strain K-12";  
RL DNA Res. 8:11-22(2001).  
CC -1- FUNCTION: RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA  
CC ALGINATE REGULATORY GENE ALG82.  
CC -----  
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CC -----  
CC EMBL; L37900; AAC36933.1; -;  
DR EMBL; AE000166; AAC3711.1; -;  
DR EMBL; U82598; AAB40810.1; -;  
DR EMBL; D90701; BAA35239.1; -;  
DR EMBL; D90702; BAA35248.1; -;  
DR EMBL; AE005240; AAG54945.1; -;  
DR EMBL; AP002552; BAB34072.1; -;  
DR Ecogene; EG12637; rnk.  
KW Complete proteome.  
SQ SEQUENCE 136 AA; 14927 MW; 7043926623BA5E1E CRC64;  
  
Query Match 100.08; Score 20; DB 1; Length 136;  
Best Local Similarity 100.08; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DIDA 4  
| | | |  
Db 10 DIDA 13  
  
RESULT 24  
INL2\_DROME  
ID INL2\_DROME STANDARD; PRT; 137 AA.  
AC Q9VT51;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Probable insulin-like peptide 2 precursor (Insulin-related peptide).  
GN IRP OR CG8167.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21107400; PubMed=11179818;  
RT Vanden Broeck J.;  
RT "Neuropeptides and their precursors in the fruitfly, Drosophila  
RT melanogaster";  
RL Peptides 22:241-254(2001).  
[2]  
RC SEQUENCE FROM N.A.  
RC STRAIN-Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.  
CC -----  
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CC -----  
CC EMBL; AJ291726; CAC17605.1; -;  
DR EMBL; AE003550; AAF50204.1; -;  
DR HSSP; P01344; IGF2.  
DR FlyBase; FBgn0036046; IRP.  
DR InterPro; IPR004825; Ins/IGF/relax.

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DR InterPro: IPR001469; ATPsynt_DE.
DR Pfam: PF00401; ATP-synt_DE; 1.
DR Pfam: PF02823; ATP-synt_DE_N; 1.
DR PRODom: PD000944; ATPsynt_DE; 1.
DR TIGRFam: TIGR01216; ATP-synt_epsi; 1.
DR Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
KW Complete proteome.
SQ SEQUENCE 140 AA; 15246 MW; 8D71A8A16566EC9D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
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DB 90 DLDA 93

RESULT 26
Y4JK_RHISN
ID Y4JK_RHISN STANDARD; PRT; 140 AA.
AC P35511;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Putative plasmid stability protein Y4JK.
DE Y4JK.
GN Rhizobium sp. (strain NGR234).
OS Rhizobium sp.
OG Plasmid sym PNGK234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OC NCBI_TaxID=394;
EN 11
RX SEQUENCE FROM N.A.
RA MEDLINE=97305956; Pubmed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RA "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -1- FUNCTION: INVOLVED IN PLASMID STABILITY (POTENTIAL).
CC -1- SIMILARITY: STRONG, TO P. SYRINGAE (PV. TOMATO) PLASMID STABILITY
CC PROTEIN STTB. ALSO STRONG, TO A. GONORHOEAE ORF CAPABLE OF
CC INHIBITING GONOCOCCAL TRANSFORMATION (PGC22).
CC -----
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CC -----
DR EMBL: AE000080; AAB91723.1; -.
DR InterPro: IPR002716; PIN.
DR Pfam: PF01850; PIN; 1.
KW Hypothetical protein; plasmid.
SQ SEQUENCE 140 AA; 15119 MW; 9142E3F8C2BFCD0C CRC64;

Query Match 100.0%; Score 20; DB 1; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
    ||||
DB 79 DLDA 82

RESULT 27
YK24_PSEAE
ID YK24_PSEAE STANDARD; PRT; 140 AA.
AC P32205; Q91290;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

16-OCT-2001 (Rel. 40, Last annotation update)  
 Hypothetical protein PA2024.  
 Pseudomonas aeruginosa.  
 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 Pseudomonas.  
 NCBI\_TaxID=287;  
 [1]  
 SEQUENCE FROM N.A.  
 STRAIN=ATCC 15692 / PA01;  
 MEDLINE=20437337; PubMed=10984043;  
 Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 opportunistic pathogen.";  
 Nature 405:959-964(2000).  
 [2]  
 SEQUENCE OF 1-28 FROM N.A.  
 STRAIN=PA08;  
 MEDLINE=91194546; PubMed=1849605;  
 Perry A.C.F., Ni Bhriain N., Brown N.L., Rouch D.A.;  
 "Molecular characterization of the gor gene encoding glutathione  
 reductase from Pseudomonas aeruginosa: determinants of substrate  
 specificity among pyridine nucleotide-disulphide oxidoreductases.";  
 Mol. Microbiol. 5:163-171(1991).  
 -----  
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 -----  
 EMBL; AE004629; AAG05412.1; -  
 EMBL; X54201; CAA38121.1; -  
 PIR; S15235; S15235.  
 InterPro; IPR004360; Gly\_bleo\_dlox.  
 Pfam; PF00903; Glyoxalase; 1.  
 Hypothetical protein; Complete proteome.  
 SEQUENCE 140 AA; 15373 MW; 26221B19B328F38 CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DIDA 4  
 Db 14 DIDA 17  
 RESULT 28  
 DTD\_STRCO  
 ID DTD\_STRCO STANDARD; PRT; 141 AA.  
 AC Q9K4F6;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE D-tyrosyl-tRNA(Tyr) deacylase (EC 3.1.-.-).  
 DTD OR SC04182 OR SC06619C.  
 GN Streptomyces coelicolor.  
 OS Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;  
 OC Actinomycetales; Streptomycetaceae; Streptomyces.  
 OC NCBI\_TaxID=1902;  
 RN [1]  
 SEQUENCE FROM N.A.  
 STRAIN=A3(2) / M145;  
 MEDLINE=21996410; PubMed=12000953;  
 Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 Hopwood D.A.;  
 "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2).";  
 Nature 415:411-417(2002).  
 CC -!- FUNCTION: Hydrolyzes D-tyrosyl-tRNA(Tyr) into D-tyrosine and free  
 tRNA(Tyr). Could be a defense mechanism against a harmful effect  
 of D-tyrosine (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -!- SIMILARITY: BELONGS TO THE DTD FAMILY.  
 -----  
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 -----  
 EMBL; AL358692; CAB94086.1; -  
 HSSP; P32147; 1JKE.  
 InterPro; IPR003732; DUF154.  
 Pfam; PF02580; DUF154; 1.  
 TIGRFAMs; TIGR00256; TIGR00256; 1.  
 KW Hydrolase; Complete proteome.  
 SQ SEQUENCE 141 AA; 14968 MW; 55F42ECAAF299E37 CRC64;  
 Query Match 100.0%; Score 20; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DIDA 4  
 Db 64 DIDA 67  
 RESULT 29  
 HBA3\_XENLA  
 ID HBA3\_XENLA STANDARD; PRT; 141 AA.  
 AC P06636;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hemoglobin alpha-3 chain (Alpha-T3).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=85297748; PubMed=2993998;  
 RA Banville D., Williams J.G.;  
 RT "The pattern of expression of the Xenopus laevis tadpole alpha-globin  
 genes and the amino acid sequence of the three major tadpole alpha-  
 globin polypeptides.";  
 Nucleic Acids Res. 13:5407-5421(1985).  
 RL -!- FUNCTION: THIS IS A LARVAL (TADPOLE) ALPHA-GLOBIN.  
 CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -!- TISSUE SPECIFICITY: Red blood cells.  
 CC -!- POLYMORPHISM: ALPHA T3 MAY BE AN ALLELE OF ALPHA T4.  
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.  
 -----  
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DR EMBL: X02796; CAA26564.1; -  
 DR PIR: A24338; A24338.  
 DR HSP: P01922; IABW.  
 DR InterPro: IPR002338; Alpha\_haem.  
 DR InterPro: IPR000971; Globin.  
 DR Pfam: PF00042; globin; 1.  
 DR PRINTS: PR00612; ALPHAHAE.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transprot; Erythrocyte.  
 FT INIT\_MET 0  
 FT METAL 58 58 IRON (HEME DISTAL LIGAND).  
 FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).  
 FT SEQUENCE 141 AA; 15303 MW; F0F1694366B7C0A7 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 Db 75 DLDA 78

RESULT 30  
 HBA3\_XENTR STANDARD; PRT; 141 AA.  
 ID P08422;  
 AC 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hemoglobin alpha-3 chain (Larval).  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 CC Xenopodinae; Silurana.  
 CC NCBI\_TaxID=8364;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=86157727; PubMed=3347501;  
 RA Knochel W., Fianne K., Beck J., Meyerhof W.;  
 RA "Nucleotide sequence of a larval alpha globin gene from Xenopus  
 RT tropicalis.";  
 RL Nucleic Acids Res. 16:1625-1625(1988).  
 CC -!- FUNCTION: THIS IS A LARVAL (TADPOLE) ALPHA-GLOBIN.  
 CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -!- TISSUE SPECIFICITY: Red blood cells.  
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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DR EMBL: X06664; CAA29864.1; -  
 DR PIR: A28538; A28538.  
 DR HSP: P01966; 1FSX.  
 DR InterPro: IPR002338; Alpha\_haem.  
 DR InterPro: IPR000971; Globin.  
 DR Pfam: PF00042; globin; 1.  
 DR PRINTS: PR00612; ALPHAHAE.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transprot; Erythrocyte.  
 FT INIT\_MET 0  
 FT METAL 58 58 IRON (HEME DISTAL LIGAND).  
 FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).  
 FT SEQUENCE 141 AA; 15355 MW; 01C7C9F83973FCDA CRC64;

SQ

Query Match 100.0%; Score 20; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 Db 75 DLDA 78

MMS5\_MYCTU STANDARD; PRT; 142 AA.  
 ID O53785;  
 AC 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Putative membrane protein MPPS5.  
 GN MPPS5 OR RV0677C OR MT0706 OR MTV040.05C.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CC NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=H37RV;  
 RA MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE MPPS FAMILY.

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DR EMBL: AL021943; CAA17460.1; -  
 DR EMBL: AE006964; AAK44931.1; -  
 DR TIGR: MT0706; -  
 DR TubercuList; RV0677c; -  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 8 25 POTENTIAL.  
 SQ SEQUENCE 142 AA; 15248 MW; 055BD99A3F46E8F5 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 Db 75 DLDA 78

```
Db 73 DLDA 76

RESULT 32
RL1L_STRAT
ID RL1L_STRAT STANDARD; PRT; 144 AA.
AC 087085;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1890;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14888;
RX MEDLINE=98401489; PubMed=9731302;
RA Kawamoto S., Ochi K.;
RT "Comparative ribosomal protein (L11 and L30) sequence analyses of
RT several Streptomyces spp. commonly used in genetic studies.";
RT Int. J. Syst. Bacteriol. 48:597-600(1998).
RL -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; X72787; CAA51297.1; -
DR EMBL; D87846; BAA22444.1; -
DR EMBL; D87846; BAA22445.1; -
DR PIR; S32235; S32235.
DR HSSP; P29395; IMMS.
DR InterPro; IPR000911; Ribosomal_L11.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding; Antibiotic resistance.
FT VARIANT 28 31 MISSING (IN THIOPEPTIN RESISTANCE).
SQ SEQUENCE 144 AA; 15032 MW; D70E8D7FDCD68122 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
| | | |
DB 123 DLDA 126

RESULT 34
RL1L_STRSQ
ID RL1L_STRSQ STANDARD; PRT; 144 AA.
AC Q07975;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK.
OS Streptomyces sp. (strain FRI-5).
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93281414; PubMed=8506151;
RA Ruengjitchachawalya M., Okamoto S., Nihira T., Yamada M.;
RT "Nucleotide sequence of the genes encoding L11 and L1 equivalent
RT ribosomal protein from Streptomyces sp. FRI-5.";
RT Nucleic Acids Res. 21:2524-2524(1993).
RL -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L11P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; AB005914; BAA31981.1; -
DR HSSP; P29395; IMMS.
DR InterPro; IPR000911; Ribosomal_L11.
DR Pfam; PF00298; Ribosomal_L11; 1.
DR ProDom; PD001367; Ribosomal_L11; 1.
DR PROSITE; PS00359; RIBOSOMAL_L11; 1.
KW Ribosomal protein; RNA-binding.
SQ SEQUENCE 144 AA; 15232 MW; 7820A6BCC9B45EA3 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
| | | |
DB 123 DLDA 126

RESULT 33
RL1L_STRGR
ID RL1L_STRGR STANDARD; PRT; 144 AA.
AC P36258; O32448;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L11.
GN RPLK OR RELC.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=94314177; PubMed=8039667;
RA Kuberski S., Kasberg T., Distler J.;
RT "The nusG gene of Streptomyces griseus: cloning of the gene and
```

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CC -----  
DR EMBL: D14451; BAA03346.1; -;  
DR PIR: S40772; S40772.  
DR HSP: P29395; LMMS.  
DR InterPro: IPR000911; Ribosomal\_L11.  
DR Pfam: PF00298; Ribosomal\_L11; 1.  
DR ProDom: PD001367; Ribosomal\_L11; 1.  
DR PROSITE: PS00359; RIBOSOMAL\_L11; 1.  
KW Ribosomal protein; RNA-binding.  
SQ SEQUENCE 144 AA; 15328 MW; A66FB987D202E6 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 123 DLDA 126

RESULT 35  
RBFA\_RHILO  
ID RBFA\_RHILO STANDARD; PRT; 146 AA.  
AC Q98BI7;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribosome-binding factor A.  
GN RBFA OR MLR5557.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;

CC [1]  
CC SEQUENCE FROM N.A.  
CC STRAIN=MAFF303099;  
CC MEDLINE=21082930; PubMed=11214968;  
CC Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
CC Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
CC Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
CC Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
CC Takeuchi C., Yamada M., Tabata S.;  
CC "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
CC Mesorhizobium loti";  
CC DNA Res. 7:331-338(2000).  
CC -1- FUNCTION: Associates with free 30S ribosomal subunits (but not  
CC with 30S subunits that are part of 70S ribosomes or polysomes).  
CC Essential for efficient processing of 16S rRNA. May interact with  
CC the 5'terminal helix region of 16S rRNA (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -1- SIMILARITY: BELONGS TO THE RBFA FAMILY.

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CC -----  
DR EMBL: AP003006; BAB51985.1; -;  
DR InterPro: IPR000238; Rib\_bind\_factA.  
DR Pfam: PF02033; RBFA; 1.  
DR ProDom: PD007327; Rib\_bind\_factA; 1.  
DR TIGRFAMs: TIGR00082; rbfa; 1.  
DR PROSITE: PS01319; RBFA; 1.  
KW rRNA processing; Complete proteome.  
SQ SEQUENCE 146 AA; 16416 MW; 3E114115F74CEFA7 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
||||  
DB 126 DLDA 129

RESULT 36  
GLBP\_CHITH  
ID GLBP\_CHITH STANDARD; PRT; 152 AA.  
AC P11582;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Globin CTT-E/E' precursor.  
GN CTT-E AND CTT-E'  
OS Chironomus thummi thummi (Midge).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;  
OC Chironomidae; Chironomidae; Chironominae; Chironomus.  
OX NCBI\_TaxID=7155;

CC [1]  
CC SEQUENCE FROM N.A.  
CC MEDLINE=88056313; PubMed=3678833;  
CC Antoine M., Erbil C., Muench E., Schnell S., Niessing J.;  
CC "Genomic organization and primary structure of five homologous pairs  
CC of intron-less genes encoding secretory globins from the insect  
CC Chironomus thummi thummi";  
CC Gene 56:41-51(1987).  
CC [2]

CC SEQUENCE FROM N.A.  
CC Hankeln T., Amid C., Weich B., Schmidt E.R.;  
CC Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.

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CC -----  
DR EMBL: M17604; AAA28253.1; -;  
DR EMBL: M17695; AAA28258.1; -;  
DR EMBL: Y10622; CAA71643.1; -;  
DR HSP: P02229; LECA.  
DR InterPro: IPR002336; Erythcrurin.  
DR InterPro: IPR000971; Globin.  
DR Pfam: PF00042; globin; 1.  
DR PRINTS: PR00611; ERYTHCRURIN.  
DR PROSITE: PS01033; GLOBIN; 1.  
KW Heme; Oxygen transport; Transport; Signal.  
FT SIGNAL 1 15  
FT CHAIN 16 152 GLOBIN CTT-E/E'.  
FT METAL 73 73 IRON (HEME DISTAL LIGAND)  
FT FT (BY SIMILARITY).  
FT METAL 102 102 IRON (HEME PROXIMAL LIGAND)  
FT FT (BY SIMILARITY).  
SQ SEQUENCE 152 AA; 15964 MW; 52D70B8CF57CFA9E CRC64;

Query Match 100.0%; Score 20; DB 1; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
||||  
DB 60 DLDA 63

RESULT 37  
RS15\_ARATH  
ID RS15\_ARATH STANDARD; PRT; 152 AA.

Q08112;  
01-FEB-1995 (Rel. 31, Created)  
01-FEB-1995 (Rel. 31, Last sequence update)  
15-JUN-2002 (Rel. 41, Last annotation update)  
40S ribosomal protein S15.  
RPS15 OR RIG OR AT1G04270 OR F19P19.26.  
Arabidopsis thaliana (Mouse-ear cress).  
Eukaryota; Viridiplantae; Streptophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
NCBI\_TaxID=3702;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=94060094; PubMed=7916644;  
Sangwan V., Lenvik T.R., Gantt S.;  
"The Arabidopsis thaliana ribosomal protein S15 (rig) gene.";  
Biochim. Biophys. Acta 1216:221-226(1993).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=cv. Columbia;  
Grellet F., Cooke R., Laudie M., Raynal M., Delseny M.;  
Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
[3]  
SEQUENCE FROM N.A.  
STRAIN=cv. Columbia;  
MEDLINE=21016719; PubMed=11130712;  
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
White O., Alonso J., Alcafi H., Araujo R., Bowman C.L., Brooks S.Y.,  
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,  
Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzali A.,  
Militischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
"Sequence and analysis of chromosome 1 of the plant Arabidopsis  
thaliana.";  
Nature 408:816-820(2000).  
[4]  
SEQUENCE OF 105-152 FROM N.A.  
STRAIN=cv. Columbia;  
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;  
Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.  
-1- SUBCELLULAR LOCATION: Cytoplasmic.  
-1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
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EMBL; Z23161; CAAB0679.1; -  
EMBL; Z23162; CAAB0681.1; -  
EMBL; X91962; CAAB3028.1; -  
EMBL; AC000104; BAB70449.1; -  
EMBL; Z17791; CAAY9070.1; -  
PIR; S34016; S34016.  
PIR; S43410; S43410.  
HSSP; P80381; 1QKF.  
InterPro: IPR002222; Ribosomal\_S19.  
Pfam: PF00203; Ribosomal\_S19; 1.  
PRINTS; PR00975; Ribosomal\_S19; 1.  
ProDom; PD001012; Ribosomal\_S19; 1.  
DR EMBL; Z23161; CAAB0679.1; -  
DR EMBL; Z23162; CAAB0681.1; -  
DR EMBL; X91962; CAAB3028.1; -  
DR EMBL; AC000104; BAB70449.1; -  
DR EMBL; Z17791; CAAY9070.1; -  
DR PIR; S34016; S34016.  
DR PIR; S43410; S43410.  
DR HSSP; P80381; 1QKF.  
DR InterPro: IPR002222; Ribosomal\_S19.  
DR Pfam; PF00203; Ribosomal\_S19; 1.  
DR PRINTS; PR00975; Ribosomal\_S19; 1.  
DR ProDom; PD001012; Ribosomal\_S19; 1.

DR TIGRFAMS; TIGR01025; rpss\_arch; 1.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; 1.  
KW Ribosomal protein.  
FT CONFLICT 2 93 A -> G (IN REF. 2).  
FT CONFLICT 93 V -> L (IN REF. 2).  
SQ SEQUENCE 152 AA; 17129 MW; D99F473432C410EC CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 28 DLDA 31  
RESULT 39  
RS15\_PODAN STANDARD; PRT; 152 AA.  
ID RS15\_PODAN  
AC P34737;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 40S ribosomal protein S15 (S12).  
GN RPS15 OR AS1.  
OS Podospora anserina.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariales; Lasiosphaeriaceae; Podospora.  
OX NCBI\_TaxID=5145;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=s;  
RX MEDLINE=94253048; PubMed=8195128;  
RA Dequard-Chablat M., Seilem C.H.;  
RT "The S12 ribosomal protein of Podospora anserina belongs to the S19  
bacterial family and controls the mitochondrial genome integrity  
through cytoplasmic translation.";  
RL J. Biol. Chem. 269:14951-14956(1994).  
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.  
-----  
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-----  
EMBL; Z23267; CAAB0805.1; -  
DR PIR; S37171; S37171.  
DR HSSP; P80381; 1QKF.  
DR InterPro: IPR002222; Ribosomal\_S19.  
DR Pfam; PF00203; Ribosomal\_S19; 1.  
DR PRINTS; PR00975; Ribosomal\_S19; 1.  
DR ProDom; PD001012; Ribosomal\_S19; 1.  
DR TIGRFAMS; TIGR01025; rpss\_arch; 1.  
DR PROSITE; PS00323; RIBOSOMAL\_S19; 1.  
KW Ribosomal protein.  
SQ SEQUENCE 152 AA; 17384 MW; 401289AA3ED9F92F CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 152;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 28 DLDA 31  
RESULT 39  
Y194\_AQUAE STANDARD; PRT; 154 AA.  
ID Y194\_AQUAE  
AC O66575;



```
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_194.
GN AQ_194.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
CC -----
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CC -----
DR EMBL; AE000677; AAC06532.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 154 AA; 18089 MW; 0FCF78184C85ADC5 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIDA 4
    ||||
Db 126 DIDA 129

RESULT 40
DUT_CAUCR STANDARD; PRT; 155 AA.
AC Q9A253;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
DE (dUTPase) (dUTP pyrophosphatase).
GN DUT OR CC3713.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- FUNCTION: This enzyme is involved in nucleotide metabolism: it
CC produces dUMP, the immediate precursor of thymidine nucleotides
CC and it decreases the intracellular concentration of dUTP so that
CC uracil cannot be incorporated into DNA (By similarity).
CC -!- CATALYTIC ACTIVITY: dUTP + H(2)O = dUMP + diphosphate.
CC -----
```

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CC -!- PATHWAY: De novo synthesis of thymidylate.
CC -!- SIMILARITY: BELONGS TO THE DUTPASE FAMILY.
CC -----
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CC -----
DR EMBL; AE006029; AAK25675.1; -
DR HSSP; P06968; 1EUF.
DR TIGR; CC3713; -
DR InterPro; IPR001428; DeoxyUTPase.
DR Pfam; PF00692; dUTPase; 1.
DR ProDom; PD000946; DeoxyUTPase; 1.
DR TIGRFAMs; TIGR00576; dut; 1.
KW Hydrolase; Nucleotide metabolism; Complete proteome.
SQ SEQUENCE 155 AA; 16215 MW; 534EC085942C4118 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DIDA 4
    ||||
Db 139 DIDA 142

RESULT 41
YS51_MYCTU STANDARD; PRT; 156 AA.
AC O05808;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein RV2851c.
GN RV2851C OR MT2917 OR MTCY24A1.06.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.
CC -----
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DR EMBL; Z95207; CAB08455.1; -  
 DR EMBL; AE007116; AAK47243.1; -  
 DR TIGR; MT2917; -  
 DR TubercuList; Rv2851c; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 156 AA; 17670 MW; 6ECBAE9F33FB365E CRC64;

Query Match 100.0%; Score 20; DB 1; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 DB 12 DLDA 15  
 ||||  
 ||||

## RESULT 42

YE19\_MYCTU STANDARD; PRT; 157 AA.  
 ID YE19\_MYCTU  
 AC P71688;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein Rv1419.  
 GN Rv1419 OR MT1462 OR MTCY21B4.37.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=H37RV;  
 RC MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OshKosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.  
 -----

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DR EMBL; Z80108; CAB02167.1; -  
 DR EMBL; AE007017; AAK45727.1; -

DR TIGR; MT1462; -  
 DR TubercuList; Rv1419; -  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 2.  
 DR SMART; SM00458; RICIN; 1.  
 DR PROSITE; PS0231; RICIN\_B\_LECTIN; 1.  
 KW Hypothetical protein; Transmembrane; Lectin; Complete proteome.  
 FT TRANSMEM 6 26 POTENTIAL.  
 FT DOMAIN 33 157 RICIN B-TYPE LECTIN.  
 SQ SEQUENCE 157 AA; 16853 MW; 35CB2E952788773D CRC64;

Query Match 100.0%; Score 20; DB 1; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 DB 122 DLDA 125  
 ||||  
 ||||

## RESULT 43

ATPX\_SYNP6 STANDARD; PRT; 158 AA.  
 ID ATPX\_SYNP6  
 AC P08446;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ATP synthase B' chain (EC 3.6.3.14) (Subunit II).  
 GN ATPG.  
 OS Synecococcus sp. (strain PCC 6301) (Anacystis nidulans).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.  
 OX NCBI\_TaxID=1139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87311713; PubMed=3041005;  
 RA Cozens A.L., Walker J.E.;  
 RT "The organization and sequence of the genes for ATP synthase subunits  
 RT in the cyanobacterium Synecococcus 6301. Support for an  
 RT endosymbiotic origin of chloroplasts."  
 RL J. Mol. Biol. 194:359-383(1987).  
 CC -1- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM OF  
 CC B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) -> ADP + phosphate +  
 CC H(+)(Out).  
 CC -1- SUBUNIT: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT  
 CC (CF0) SUBUNIT OF THE ATPASE COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.  
 -----

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 -----

DR EMBL; X05302; CAA28925.1; -  
 DR PIR; X10828; LWYCB8.  
 DR InterPro; IPR002146; ATPsynth\_B/B'sub.  
 DR Pfam; PF00430; ATP-synt\_B; 1.  
 KW Hydrogen ion transport; Transmembrane; CF(0).  
 SQ SEQUENCE 158 AA; 17412 MW; 60A5896390DC38E0 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 DB 21 DLDA 24  
 ||||  
 ||||

## RESULT 44

ATPX\_ANASP  
ID ATPX\_ANASP STANDARD; PRT; 163 AA.  
AC P12410;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE ATP synthase B' chain (EC 3.6.3.14) (Subunit II).  
GN ATPG OR ALL0008.  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88298650; PubMed=2900236;  
RA McCarr D.F., Whitaker R.A., Alam J., Vrba J.M., Curtis S.E.;  
RT "Genes encoding the alpha, gamma, delta, and four F0 subunits of ATP  
synthase constitute an operon in the cyanobacterium Anabaena sp.  
strain PCC 7120.";  
RL J. Bacteriol. 170:3448-3458(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakazaki N., Shimp S., Sugimoto M., Takazawa M., Yamada M.,  
RA Yasuda M., Tabata S.;  
RT "Complete genomic sequence of the filamentous nitrogen-fixing  
cyanobacterium Anabaena sp. strain PCC 7120.";  
RL DNA Res. 8:205-213(2001).  
CC -!- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM OF  
CC B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.  
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
CC H(+) (Out).  
CC -!- SUBUNIT: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT  
CC (CF(0) SUBUNIT) OF THE ATPASE COMPLEX.  
CC -!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.  
CC -----  
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CC -----  
DR EMBL; AF242564; AAA21988.1; -;  
DR EMBL; AF003581; BAB77532.1; -;  
DR PIR; D31090; D31090.  
DR InterPro; IPR002146; ATPsynt\_B/B' sub.  
DR Pfam; PF00430; ATP-synt\_B; 1.  
KW Hydrogen ion transport; Transmembrane; CF(0); Complete proteome.  
SQ SEQUENCE 163 AA; 17972 MW; E48D1D0F9C4BA705 CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 163;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 21 DLDA 24  
RESULT 45  
FUSE\_BURCE  
ID FUSE\_BURCE STANDARD; PRT; 168 AA.  
AC P24130;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE Fusaric acid resistance protein|fuse.  
GN FUSE.  
OS Burkholderia cepacia (Pseudomonas cepacia).  
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;  
Burkholderia.  
OC NCBI\_TaxID=292;  
OX [1]  
RN SEQUENCE FROM N.A.  
RX STRAIN=UK1;  
RX MEDLINE=92109974; PubMed=1370369;  
RA Utsumi R., Yagi T., Katayama S., Katsuragi K., Tachibana K.,  
RA Toyoda H., Ouchi S., Obata K., Shibano Y., Noda M.;  
RT "Molecular cloning and characterization of the fusaric  
acid-resistance gene from Pseudomonas cepacia.";  
RL Agric. Biol. Chem. 55:1913-1918(1991).  
CC -!- FUNCTION: INVOLVED IN THE RESISTANCE (DETOXIFICATION) OF THE  
CC FUNGAL TOXIN FUSARIC ACID.  
CC -----  
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CC -----  
DR EMBL; S77489; AAC60392.1; -;  
DR EMBL; D12503; BAA02068.1; -;  
DR PIR; JS0513; JS0513.  
SQ SEQUENCE 168 AA; 18484 MW; 5197296234AFBA5E CRC64;  
Query Match 100.0%; Score 20; DB 1; Length 168;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DLDA 4  
Db 35 DLDA 38  
Search completed: February 6, 2003, 11:16:44  
Job time : 7.33333 secs

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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 21.3333 Seconds  
(without alignments)  
38.634 Million cell updates/sec

Title: PAT943-2

Perfect score: 20

Sequence: 1 dlda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4211

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	30	17 Q8ZVL0	Q8ZVL0 pyrobaculum
2	20	100.0	31	2 Q9S5Z5	Q9S5Z5 streptomyces
3	20	100.0	48	4 Q75253	Q75253 homo sapien
4	20	100.0	49	2 Q8RMK4	Q8RMK4 corynebacte
5	20	100.0	51	5 Q26905	Q26905 trichostro
6	20	100.0	54	12 Q99175	Q99175 porcine ent
7	20	100.0	55	2 Q9XC71	Q9XC71 salmonella
8	20	100.0	55	12 Q84995	Q84995 eastern equ
9	20	100.0	56	10 Q9M615	Q9M615 vitis ripar
10	20	100.0	60	17 Q8ZVG7	Q8ZVG7 pyrobaculum
11	20	100.0	61	16 Q53965	Q53965 streptomyces
12	20	100.0	62	16 Q9ZS16	Q9ZS16 rhizobium m
13	20	100.0	63	10 Q9SPN4	Q9SPN4 oryza sativ
14	20	100.0	65	2 Q54732	Q54732 synecococc
15	20	100.0	66	16 Q50486	Q50486 streptomyces
16	20	100.0	67	2 Q9L8X2	Q9L8X2 streptomyces

17	20	100.0	67	2 Q9L8X0	Q9L8X0 streptomyces
18	20	100.0	69	2 Q9KIL3	Q9KIL3 streptomyces
19	20	100.0	69	16 Q9CIA6	Q9CIA6 lactococcus
20	20	100.0	70	6 Q9TR16	Q9TR16 bos taurus
21	20	100.0	70	10 Q9LD48	Q9LD48 arabidopsis
22	20	100.0	70	16 Q9ZK57	Q9ZK57 rhizobium m
23	20	100.0	71	16 Q69718	Q69718 mycobacteri
24	20	100.0	72	16 Q9ZS57	Q9ZS57 rhizobium m
25	20	100.0	74	12 Q9YWG7	Q9YWG7 epiphyas po
26	20	100.0	74	16 Q99YD3	Q99YD3 streptococc
27	20	100.0	74	16 Q9FBC6	Q9FBC6 streptococc
28	20	100.0	74	16 Q99QG6	Q99QG6 streptomyces
29	20	100.0	75	2 Q93EG1	Q93EG1 helicobacte
30	20	100.0	75	6 P79246	P79246 sus scrofa
31	20	100.0	75	10 P93274	P93274 malus domes
32	20	100.0	75	12 Q85323	Q85323 vaccinia v1
33	20	100.0	76	12 Q9Q8W0	Q9Q8W0 shope fibro
34	20	100.0	76	13 Q90T04	Q90T04 poephila gu
35	20	100.0	76	16 Q86536	Q86536 streptomyces
36	20	100.0	77	2 Q9AN31	Q9AN31 bradyrhizob
37	20	100.0	77	16 Q9F7T4	Q9F7T4 streptococc
38	20	100.0	78	16 Q92NC0	Q92NC0 rhizobium m
39	20	100.0	79	9 Q9A298	Q9A298 lactobacill
40	20	100.0	79	16 Q25449	Q25449 helicobacte
41	20	100.0	79	16 Q9ZL89	Q9ZL89 helicobacte
42	20	100.0	79	16 Q9A5F8	Q9A5F8 caulobacter
43	20	100.0	79	16 Q9AOC1	Q9AOC1 streptococc
44	20	100.0	79	16 Q926P1	Q926P1 listeria in
45	20	100.0	80	2 Q9LB27	Q9LB27 chesapeake

#### ALIGNMENTS

#### RESULT 1

Q8ZVL0 PRELIMINARY; PRT; 30 AA.  
 AC Q8ZVL0;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE PaREP2b.  
 GN PAE2231.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 OC Thermoproteaceae; Pyrobaculum.  
 OX NCBI\_TaxID=13773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;  
 RX PubMed=11792869;  
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
 RA Miller J.H.;  
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
 aerophilum";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
 DR EMBL; AE009864; AAL64046.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 30 AA; 3535 MW; 16301757DB3B1468 CRC64;

Query Match 100.0%; Score 20; DB 17; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
 Db 7 DLDA 10  
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#### RESULT 2

Q9S5Z5 PRELIMINARY; PRT; 31 AA.  
 ID Q9S5Z5  
 AC Q9S5Z5;

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE RNase P protein (Fragment).  
GN RNPA.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=3A(2);  
RA Cal-Mor O., Borovok I., Cohen G., Aharonowitz Y.;  
RT "Gene organization in the trxB/A/oriC region of the Streptomyces  
coelicolor 3A(2) chromosome and comparison with other bacteria";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF031590; AAC03489.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 31 AA; 3069 MW; 709BE4DA5CAAB6E5 CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 17 DLDA 20  
|||||  
  
RESULT 3  
O75253 PRELIMINARY; PRT; 48 AA.  
ID O75253;  
AC O75253;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE R31341\_2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,  
RA Burkhardt-Schultz K., Gordon L., Ramirez M., Stillwagen S.,  
RA Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,  
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,  
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
RA Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
RA Kobayashi A., Olsen A.S., Carrano A.V.;  
RT "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a  
serine protease gene cluster";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC005331; AAC27666.1; -;  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rrm; 1.  
DR PROSITE; PS50102; RRM; 1.  
FT NON\_TER 48  
SQ SEQUENCE 48 AA; 5689 MW; 98DF39514911566A CRC64;  
  
Query Match 100.0%; Score 20; DB 4; Length 48;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 3 DLDA 6  
|||||  
  
RESULT 4  
Q8RMK4 PRELIMINARY; PRT; 49 AA.  
ID Q8RMK4

Q8RMK4;  
AC 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE ORF1.  
OS Corynebacterium diphtheriae.  
OG Plasmid pNG2.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;  
OC Corynebacterium.  
OX NCBI\_TaxID=1717;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S601;  
RA Tauch A., Bischoff N., Kalinowski J., Puehler A.;  
RT "Insights into the genetic organization of the Corynebacterium  
diphtheriae erythromycin resistance plasmid pNG2 deduced from its  
complete nucleotide sequence.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF492560; AAM12761.1; -;  
KW Plasmid.  
SQ SEQUENCE 49 AA; 5396 MW; E4F2A47F4DB7C895 CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 49;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 15 DLDA 18  
|||||  
  
RESULT 5  
Q26905 PRELIMINARY; PRT; 51 AA.  
ID Q26905;  
AC Q26905;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Beta-tubulin (Fragment).  
GN TCB-1.  
OS Trichostyrngylus colubriformis.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Trichostyrngyloidea; Trichostyrngylidae; Trichostyrngylinae;  
OC Trichostyrngylus.  
OX NCBI\_TaxID=6319;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCMASTER;  
RA Grant W.N., Mascord L.J.;  
RT "Beta-tubulin gene polymorphism and benzimidazole resistance in  
Trichostyrngylus colubriformis";  
RL Int. J. Parasitol. 0:0-0(1995).  
DR EMBL; U39620; AAA80231.1; -;  
DR InterPro; IPR003008; Tubulin\_Ftsz.  
DR Pfam; PF00091; tubulin; 1.  
KW GTP-binding.  
FT NON\_TER 1  
SQ SEQUENCE 51 AA; 5750 MW; 78003D1CD26CE60B CRC64;  
  
Query Match 100.0%; Score 20; DB 5; Length 51;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 38 DLDA 41  
|||||  
  
RESULT 6  
Q99I75 PRELIMINARY; PRT; 54 AA.  
ID Q99I75  
AC Q99I75;

DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Capsid VP2 (Fragment).  
GN 18.

OS Porcine enterovirus 10.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Enterovirus.  
OX NCBI\_TaxID=106967;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LF54;  
RX MEDLINE=21102978; PubMed=11161281;  
RA Kaku Y., Sarai A., Murakami Y.;  
RT "Genetic reclassification of porcine enteroviruses.";  
RL J. Gen. Virol. 82:417-424(2001).  
DR EMBL; AB049562; BAB32827.1; -.  
DR HSP; P12915; IBEV.  
DR InterPro; IPR001676; Rhv.  
DR Pfam; PF00073; rhv; 1.  
FT NON\_TER 1  
FT NON\_TER 54  
SQ SEQUENCE 54 AA; 5655 MW; EC728F3DC4585BB7 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 54;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 44 DLDA 47

## RESULT 7

Q9XC71 Q9XC71 PRELIMINARY; PRT; 55 AA.  
AC Q9XC71;  
DT 01-NOV-1999 (TReMBLrel. 12, Created)  
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Aminopeptidase N (Fragment).  
GN PEPN.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SL1344;  
RA Norel F., Coyneault C., Bossi L., Figueroa-Bossi N.;  
RT "Attachment sites of Gifsy-1 and Gifsy-2 prophages in the Salmonella typhimurium chromosome.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF147699; AAD43091.1; -.  
DR MEROPS; M01.005; -.  
FT NON\_TER 55  
SQ SEQUENCE 55 AA; 6257 MW; 7C4F369F417345A3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 28 DLDA 31

## RESULT 8

Q64995 Q64995 PRELIMINARY; PRT; 55 AA.  
AC Q64995;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Eastern equine encephalomyelitis virus (South American strain) RNA 5' terminal sequence (Fragment).  
OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
OC Alphavirus.  
OX NCBI\_TaxID=11021;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83010261; PubMed=6288962;  
RA Ou J.-H., Trent D.W., Strauss J.H.;  
RT "The 3'-non-coding regions of alphavirus RNAs contain repeating sequences.";  
RL J. Mol. Biol. 156:719-730(1982).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83268700; PubMed=6308269;  
RA Ou J.-H., Strauss E.G., Strauss J.H.;  
RT "The 5' terminal sequences of the genomic RNAs of several alphaviruses.";  
RL J. Mol. Biol. 168:1-15(1983).  
DR EMBL; K00701; AAA42982.1; -.  
FT NON\_TER 55  
SQ SEQUENCE 55 AA; 6227 MW; C9E12ADDB190BCB3 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 55;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 7 DLDA 10

## RESULT 9

Q9M615 Q9M615 PRELIMINARY; PRT; 56 AA.  
AC Q9M615;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Proline rich protein 2 (Fragment).  
GN PRP2.  
OS Vitis riparia (Frost grape) (Vitis vulpina).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;  
OC Vitis.  
OX NCBI\_TaxID=96939;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=FLOWER BUDS;  
RA Li X.Z., McKersie B.D.;  
RT "Freezing tolerance in grapevines.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220197; AAF32353.1; -.  
DR HSP; P24337; 1HVP.  
DR InterPro; IPR001768; Try/amyl\_inhbr.  
DR Pfam; PF00234; tryp\_alpha\_amyl; 1.  
FT NON\_TER 1  
SQ SEQUENCE 56 AA; 5737 MW; D3E02C9CB5FC8ECE CRC64;

Query Match 100.0%; Score 20; DB 10; Length 56;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4  
Db 12 DLDA 15

## RESULT 10

Q8ZVG7

ID O8ZVG7 PRELIMINARY; PRT; 60 AA.  
AC O8ZVG7;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Hypothetical protein PAE2291.  
GN PAE2291.  
OS Pyrobaculum aerophilum.  
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
OC Thermoproteaceae; Pyrobaculum.  
OX NCBI\_TaxID=13773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;  
RX PubMed=11792869;  
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
RA Miller J.H.;  
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
RT aerophilum.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
DR EMBL: AE009868; AAL64089.1; --  
KW Hypothetical protein: Complete proteome.  
SQ SEQUENCE 60 AA; 6575 MW; 3872131892320B5D CRC64;  
  
Query Match 100.0%; Score 20; DB 17; Length 60;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 16 DLDA 19  
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RESULT 11  
Q53965 PRELIMINARY; PRT; 61 AA.  
ID Q53965;  
AC Q53965;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
DE EXCISTONASE.  
GN XIS OR SC04616 OR SCD39.16C.  
OS Streptomyces coelicolor.  
OG Plasmid pRI1724.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC PLASMID=PRI1724;  
RX MEDLINE=93259953; PubMed=8387993;  
RA Brasch M.A., Pettis G.S., Lee S.C., Cohen S.N.;  
RT "Localization and nucleotide sequences of genes mediating site-  
RT specific recombination of the SLPI element in Streptomyces lividans.";  
RL J. Bacteriol. 175:3067-3074(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Brown S.P., Harris D.;  
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapite D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
RT coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL: X71358; CAA50493.1; --  
DR EMBL: AL392146; CAC08269.1; --  
KW Plasmid.  
SQ SEQUENCE 61 AA; 7103 MW; CCC67B2F0D173512 CRC64;  
  
Query Match 100.0%; Score 20; DB 16; Length 61;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 49 DLDA 52  
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RESULT 12  
Q92S16 PRELIMINARY; PRT; 62 AA.  
ID Q92S16;  
AC Q92S16;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE Hypothetical unknown protein SMC02319.  
GN R00625 OR SMC02319.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Bountry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,  
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont  
RT Sinorhizobium meliloti strain 1021.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL: AL591784; CAC45197.1; --  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 62 AA; 7001 MW; F5F3E902AD9E669F CRC64;  
  
Query Match 100.0%; Score 20; DB 16; Length 62;  
Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 55 DLDA 58  
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|  
  
RESULT 13  
Q9SPN4 PRELIMINARY; PRT; 63 AA.  
ID Q9SPN4;  
AC Q9SPN4;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Hypothetical 6.5 kDa protein (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. IR-BB21;  
RA Han F., Kilian A., Chen J.P., Kudrna D., Steffenson B., Yamamoto K.,  
RA Matsumoto T., Sasaki T., Kleinbols A.;  
RT "Sequence analysis of a rice BAC covering the syntenous barley Rpg1  
region.";  
RL Genome 0:0-0(1999).  
DR EMBL; AF149815; AAF00148.1; -.  
DR HSSP; P24337; IHYP.  
DR InterPro; IPR001768; Try/amyl\_inhtr.  
DR Pfam; PF00234; tryp\_alpha\_amyl; 1.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 63 AA; 6506 MW; 81BA557A94EF695D CRC64;  
  
Query Match 100.0%; Score 20; DB 10; Length 63;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 19 DLDA 22  
  
RESULT 14  
Q54732 PRELIMINARY; PRT; 65 AA.  
AC Q54732;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)  
DE Synchococcus PCC7942 chromosomal region used as basis of neutral site  
DE II recombinational cloning vectors.  
OS Synchococcus sp. (strain PCC 7942) (Anacystis nidulans R2).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
OX NCBI\_TaxID=1140;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PCC 7942;  
RA Tsinoremas N.F., Golden S.S.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U44761; AAA86650.1; -.  
SQ SEQUENCE 65 AA; 7546 MW; 0CF9C805E2E55EEB CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 65;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 17 DLDA 20  
  
RESULT 15  
O50486 PRELIMINARY; PRT; 66 AA.  
AC O50486;  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Hypothetical protein SC05768.  
GN SC05768 OR SC48.07C.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Lark L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL020958; CAA15874.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 66 AA; 7391 MW; D962DA10258E6166 CRC64;  
  
Query Match 100.0%; Score 20; DB 16; Length 66;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 7 DLDA 10  
  
RESULT 16  
Q9L8X2 PRELIMINARY; PRT; 67 AA.  
AC Q9L8X2;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE Polyketide synthase module 5 (Fragment).  
OS Streptomyces venezuelae.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=54571;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC15068;  
RX MEDLINE=20179700; PubMed=10713461;  
RA Xue Y., Wilson D., Sherman D.H.;  
RT "Genetic architecture of the polyketide synthases for methymycin and  
pikromycin series macrolides.";  
RL Gene 245:203-211(2000).  
DR EMBL; AF193251; AAF61859.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 67 AA; 6905 MW; 9A8A2E2F8EC1DF97 CRC64;  
  
Query Match 100.0%; Score 20; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLDA 4  
Db 51 DLDA 54  
  
RESULT 17  
Q9L8X0 PRELIMINARY; PRT; 67 AA.  
AC Q9L8X0;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE Polyketide synthase module 5 (Fragment).  
OS Streptomyces narbonensis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

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OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
RX NCBI_TaxID=67333;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=ATCC19790;
RA MEDLINE=20179700; PubMed=107113461;
RX Xue Y., Wilson D., Sherman D.H.;
RA "Genetic architecture of the polyketide synthases for methymycin and
RT pikromycin series macrolides.";
RL Gene 245:203-211(2000).
DR EMBL; AF193252; AAF61861.1; -.
FT NON_TER
SQ SEQUENCE 67 AA; 6841 MW; B7358A8954E4ED59 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 51 DLDA 54

RESULT 18
Q9KIL3 PRELIMINARY; PRT; 69 AA.
AC Q9KIL3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE F132r (Fragment).
GN F132r.
OS Streptomyces coelicolor A3(2).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=100226;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=M145;
RA Kormanec J., Sevcikova B., Homerova D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF230493; AAF82067.1; -.
FT NON_TER
SQ SEQUENCE 69 AA; 7611 MW; F824D0F3BCECD7F9 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 58 DLDA 61

RESULT 19
Q9CIA6 PRELIMINARY; PRT; 69 AA.
AC Q9CIA6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Prophage pil protein 25.
GN P125 OR LL0460.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=IL1403;
RA MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;

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RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
DR EMBL; AE006282; AAK04558.1; -.
KW Complete proteome.
SQ SEQUENCE 69 AA; 7893 MW; 2689487DF9E968E1 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 41 DLDA 44

RESULT 20
Q9TR16 PRELIMINARY; PRT; 70 AA.
ID Q9TR16;
AC Q9TR16;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE CORNEA-associated antigen, CO-AG-CALGRANULIN C homolog.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96181454; PubMed=8603881;
RA Liu S.H., Gottsch J.D.;
RT "Amino acid sequence of an immunogenic corneal stromal protein.";
RL Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
DR HSSP; P80511; 1E8A.
DR InterPro; IPR001751; CaBP_S100.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF01023; S_100; 1.
DR ProDom; PD003407; CaBP_S100; 1.
DR PROSITE; PS003407; CaBP_S100; 1.
SQ SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 59 DLDA 62

RESULT 21
Q9LD48 PRELIMINARY; PRT; 70 AA.
ID Q9LD48;
AC Q9LD48;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE F14M2.2 protein (T3M13.13 protein).
GN F14M2.2 OR T3M13.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

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RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. COLOMBIA;  
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,  
RA Matti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,  
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.,  
RT "Arabidopsis thaliana chromosome 1 BAC T3M13 genomic sequence."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC010164; AAF97294.1; -;  
DR EMBL; AC022288; AAG52205.1; -;  
SQ SEQUENCE 70 AA; 8139 MW; FC1B869C0C3534E0 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 70;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db ||||  
25 DLDA 28

RESULT 22

Q92K57  
ID Q92K57 PRELIMINARY; PRT; 70 AA.  
AC Q92K57;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein R02063.  
GN R02063 OR SMC04324.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
OX NCBI\_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Godrie T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,  
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.,  
RT "Analysis of the chromosome sequence of the legume symbiont  
Sinorhizobium meliloti strain 1021".  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591789; CAC46642.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 70 AA; 7140 MW; 6243942B93F1C99 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 70;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db ||||  
46 DLDA 49

RESULT 23

O69718  
ID O69718 PRELIMINARY; PRT; 71 AA.  
AC O69718;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Putative integrase fragment.  
GN RV3751 OR MTV025.099.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaiia F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Stulton J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
complete genome sequence."  
RL Nature 393:537-544(1998).  
DR EMBL; AL022121; CAA18073.1; -;  
DR Tuberculist; RV3751; -;  
DR InterPro; IPR002104; Phage\_integrase.  
DR Pfam; PF00589; Phage\_integrase; 1.  
KW Complete proteome.  
SQ SEQUENCE 71 AA; 7584 MW; 4682AFA99F5D8145 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 71;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db ||||  
55 DLDA 58

RESULT 24

Q92S57  
ID Q92S57 PRELIMINARY; PRT; 72 AA.  
AC Q92S57;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein R00570.  
GN R00570 OR SMC02266.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
OX NCBI\_TaxID=382;

RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,  
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.,  
RT "Analysis of the chromosome sequence of the legume symbiont  
Sinorhizobium meliloti strain 1021".  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591784; CAC45142.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 72 AA; 7854 MW; 14D2ECF82376DC9 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 72;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
Db ||||  
34 DLDA 37

RESULT 25

Q9YW97  
ID Q9YW97 PRELIMINARY; PRT; 74 AA.  
AC Q9YW97;

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DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Capsid protein homolog (Fragment).
OS Epiphyas postvittana nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=70600;
RN [1]
RP SEQUENCE FROM N.A.
RA Hyink O., Graves S., Fairbairn F.M., Ward V.K.;
RT "Mapping and Polyhedrin Gene Analysis of the Epiphyas postvittana
RL Nucleopolyhedrovirus Genome.";
RL J. Gen. Virol. 78:2853-2862(1998).
DR EMBL; AF061578; AAC72190.1; -
FT NON_TER 1
SQ SEQUENCE 74 AA; 8484 MW; 272B27213A310078 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 68 DLDA 71

RESULT 26
Q99YD3 PRELIMINARY; PRT; 74 AA.
AC Q99YD3;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Acyl carrier protein (ACP).
OS ACPP OR SPV1753.
GN Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., Mshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- FUNCTION: THIS PROTEIN IS THE CARRIER OF THE GROWING FATTY ACID
CC CHAIN IN FATTY ACID BIOSYNTHESIS (BY SIMILARITY).
DR EMBL; AE006603; AAK34496.1; -
DR HSSP; P02901; IACP.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Fatty acid biosynthesis; Phosphopantetheine; Complete proteome.
SQ SEQUENCE 74 AA; 8343 MW; 41D7F7F23065B44 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 27
Q9FEC6 PRELIMINARY; PRT; 74 AA.
AC Q9FEC6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Acyl carrier protein.
OS ACPP OR SP0418.
GN Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=R6;
RX MEDLINE=20365714; PubMed=10910344;
RA Heath R.J., Rock C.O.;
RT "A triclosan-resistant bacterial enzyme.";
RL Nature 406:145-146(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AF197933; AAF98272.1; -
DR EMBL; AE007353; AAK74581.1; -
DR HSSP; P02901; IACP.
DR TIGR; SP0418; -
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Phosphopantetheine; Complete proteome.
SQ SEQUENCE 74 AA; 8268 MW; E2E9A78567090C14 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 30 DLDA 33

RESULT 28
Q99QG6 PRELIMINARY; PRT; 74 AA.
AC Q99QG6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein SCP1.348.
GN SCP1.348 AND SCP1.06C.
OS Streptomyces coelicolor.
OG Plasmid SCP1.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(2);
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

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RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL590464; CAC36873.1; -.
DR EMBL: AL590463; CAC36528.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 74 AA; 7940 MW; 48C43E8075052C08 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 11 DLDA 14

RESULT 29
Q93EG1 PRELIMINARY; PRT; 75 AA.
AC Q93EG1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative citrate synthase (Fragment).
GN GLTA.
OS Helicobacter hepaticus.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=32025;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-3B1;
RA Ge Z., Feng Y., Fox J.G.;
RT "Helicobacter hepaticus genome: construction of an ordered cosmid
RT library and sequence analysis of the selected genomic regions.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF358704; AAI16694.1; -.
DR InterPro: IPR002020; Citrate_synt.
DR Pfam: PF00285; citrate_synt; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8591 MW; 4D2DD8290D6346B3 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 17 DLDA 20

RESULT 30
P79246 PRELIMINARY; PRT; 75 AA.
AC P79246;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hormone-sensitive lipase (Fragment).
GN HSL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ADIPOSE TISSUE;
RX MEDLINE-96057569; PubMed-7549969;
RA Liu C.Y., Liang L.C., Chang L.C.;
RT "Differential responses of hormone-sensitive lipase gene to
RT nutritional transition in adipose tissue, liver, and skeletal muscle
RT of pigs.";
RL Biochem. Mol. Biol. Int. 36:689-694(1995).
DR EMBL: S80110; ABA47019.2; -.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8477 MW; 5B0B0684C98B4148 CRC64;

Query Match 100.0%; Score 20; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 9 DLDA 12

RESULT 31
P93274 PRELIMINARY; PRT; 75 AA.
AC P93274;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Proline rich protein (Fragment).
GN PRP.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRANNY SMITH;
RA Dong Y.-H., Janssen B.J., Bielecki L.L., Atkinson R.G., Morris B.A.,
RA Gardner R.C.;
RT "Isolating and characterizing genes differentially expressed early in
RT apple fruit development.";
RL J. Am. Soc. Hortic. Sci. 122:752-757(1997).
DR EMBL: U80271; AAC06386.1; -.
DR HSSP; P24337; LHYP.
DR InterPro: IPR003612; AAI.
DR InterPro: IPR001768; Try/amyl_inhbtr.
DR Pfam: PF00234; tryp_alpha_amyl; 1.
DR SMART; SM00499; AAI; 1.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 7643 MW; 694B833A59D8AD6F CRC64;

Query Match 100.0%; Score 20; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 31 DLDA 34

RESULT 32
Q85323 PRELIMINARY; PRT; 75 AA.
AC Q85323;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE D5R protein (Fragment).
GN D5R.
OS Vaccinia virus.
```

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IHD-W;  
RX MEDLINE=94120724; PubMed=8291232;  
RA Millon A.K., Carpenter M.S., DeLange A.M.;  
RT "the vaccinia virus-encoded uracil DNA glycosylase has an essential  
role in viral DNA replication.";  
RL Virology 198:504-513(1994).  
DR EMBL; L24385; AAA18016.2; -.  
DR InterPro; IPR004968; Pox\_D5.  
DR Pfam; PF03288; Pox\_D5; 1.  
FT NON\_TER 75  
SQ SEQUENCE 75 AA; 8648 MW; 884EBCBE5B9560D8 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDA 4

Db 72 DLDA 75

RESULT 33

ID OQ8W0 PRELIMINARY; PRT; 76 AA.  
AC OQ8W0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Gp118L.  
GN S118L.  
OS Shope fibroma virus (strain Kasza) (SFV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Leporipoxvirus.  
OX NCBI\_TaxID=10272;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KASZA;  
RX MEDLINE=84165064; PubMed=6323741;  
RA Delange A.M., Macaulay C., Block W., Mueller T., McFadden G.;  
RT "Tumorigenic poxviruses: construction of the composite physical map of  
the Shope fibroma virus genome.";  
RL J. Virol. 50:408-416(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KASZA;  
RX MEDLINE=92074222; PubMed=1660196;  
RA Strayer D.S., Jerng H.H., O'Connor K.;  
RT "Sequence and analysis of a portion of the genomes of Shope fibroma  
virus and malignant rabbit fibroma virus that is important for viral  
replication in lymphocytes.";  
RL Virology 185:585-595(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KASZA;  
RX MEDLINE=20032074; PubMed=10562495;  
RA Willer D.O., McFadden G., Evans D.H.;  
RT "The complete genome sequence of shope (Rabbit) fibroma virus.";  
RL Virology 264:319-343(1999).  
DR EMBL; AF170722; AAF18001.1; -.  
SQ SEQUENCE 76 AA; 8549 MW; 7E636A24EBFAC0D7 CRC64;

Query Match 100.0%; Score 20; DB 12; Length 76;

Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDA 4

Db 25 DLDA 28

RESULT 34

ID OQ0Y04 PRELIMINARY; PRT; 76 AA.  
AC OQ0Y04;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE ATP synthase alpha subunit (Fragment).  
OS Poephila guttata (Zebra finch) (Taeniopygia guttata).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;  
OC Estrilidae; Taeniopygia.  
OX NCBI\_TaxID=59729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Metzendorf R.;  
RT "Effect of inhibition of aromatase on gene expression and behavior in  
a songbird.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
GRADIENT ACROSS THE MEMBRANE (BY SIMILARITY).  
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC  
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).  
CC EMBL; AF314256; AAL26859.1; -.  
DR InterPro; IPR000793; ATPase\_a/bc.  
DR InterPro; IPR000790; ATPase\_ac.  
DR Pfam; PF00306; ATP-synt\_ab\_C; 1.  
DR ProDom; PD001099; ATPase\_ac; 1.  
KW ATP synthesis; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase.  
FT NON\_TER 1  
FT NON\_TER 76  
SQ SEQUENCE 76 AA; 8431 MW; 83EFC5ADEB84970 CRC64;

Query Match 100.0%; Score 20; DB 13; Length 76;

Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLDA 4

Db 2 DLDA 5

RESULT 35

ID O86536 PRELIMINARY; PRT; 76 AA.  
AC O86536;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical protein SC05555.  
GN SC05555 OR SC1C2.36.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2) / M145;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";

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RL Nature 417:141-147(2002).
DR EMBL; AL031124; CAA20003.1; -.
KW Hypothetical protein.
SQ SEQUENCE 76 AA; 8422 MW; 6AB2D84D0B80F560 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 65 DLDA 68

RESULT 36
Q9AN31 PRELIMINARY; PRT; 77 AA.
AC Q9AN31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE ID597.
DE ID597.
GN ID597.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=110SPC4;
RX MEDLINE=21101824; PubMed=11157954;
RA Gottfert M., Rothlisberger S., Kundig C., Beck C., Marty R.,
RA Hennecke H.;
RT "Potential symbiosis-specific genes uncovered by sequencing a 410-kb
RT DNA region of the Bradyrhizobium japonicum chromosome."
RL J. Bacteriol. 183:1405-1412(2001).
DR EMBL; AF322013; AAG60947.1; -.
SQ SEQUENCE 77 AA; 8646 MW; 6205B1062AC86D00 CRC64;

Query Match 100.0%; Score 20; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 46 DLDA 49

RESULT 37
Q9F774 PRELIMINARY; PRT; 77 AA.
AC Q9F774;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl carrier protein (Acyl carrier protein, putative).
GN ACPP OR SP0038.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20469436; PubMed=10903317;
RA McAllister K.A., Peery R.B., Meier T.I., Fischl A.S., Zhao G.;
RT "Biochemical and Molecular Analyses of the Streptococcus pneumoniae
RT Acyl Carrier Protein Synthase, an Enzyme Essential for Fatty Acid
RT Biosynthesis."
RL J. Biol. Chem. 275:30864-30872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;

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RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AF278618; AAG22707.1; -.
DR EMBL; AF007321; AAK74228.1; -.
DR TIGR; SP0038; -.
DR InterPro; IPR003880; Ppantne_attach.
DR Pfam; PF00550; pp-binding; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Phosphopantetheine; Complete proteome.
SQ SEQUENCE 77 AA; 8835 MW; 2CAB5EBE266AC256 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 33 DLDA 36

RESULT 38
Q92NC0 PRELIMINARY; PRT; 78 AA.
AC Q92NC0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein R02290.
GN R02290 OR SMC01546.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetalle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591790; CAC46869.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 78 AA; 8582 MW; 9B9ED1D2EA7A184E CRC64;

Query Match 100.0%; Score 20; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4
Db 24 DLDA 27

RESULT 39
Q9AZ98 PRELIMINARY; PRT; 79 AA.
AC Q9AZ98;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ORF79.
GN Lactobacillus johnsonii prophage Lj771.
OS Viruses.
OC NCBI_TaxID=139871;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=2045575; PubMed=10998330;
RX Desiere F., Fridmore R.D., Brussow H.;
RA "Comparative genomics of the late gene cluster from lactobacillus
RT phages.";
RL Virology 275:294-305(2000).
DR EMBL; AF195901; AAK27923.1;
SQ SEQUENCE 79 AA; 8717 MW; B2308AD37074A848 CRC64;

Query Match 100.0%; Score 20; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 32 DLDA 35

RESULT 40
O25449 PRELIMINARY; PRT; 79 AA.
AC O25449;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein HP0754.
GN HP0754.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000588; AAD07810.1;
DR TIGR; HP0754;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 79 AA; 9113 MW; DF076819852219BD CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 39 DLDA 42

RESULT 41
Q92L89 PRELIMINARY; PRT; 79 AA.
ID Q92L89
AC Q92L89
DT 01-MAY-1999 (TReMBLrel. 10, Created)

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DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE PUTATIVE.
GN JHP0691.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.D., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001500; AAD06266.1;
KW Complete proteome.
SQ SEQUENCE 79 AA; 9059 MW; DF02C6102294A6FF CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 39 DLDA 42

RESULT 42
Q9A5F8 PRELIMINARY; PRT; 79 AA.
ID Q9A5F8
AC Q9A5F8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical protein CC2492.
GN CC2492.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005918; AAK24463.1;
DR TIGR; CC2492;
DR InterPro; IPR003850; UPF0062.
DR Pfam; PF02700; UPF0062;
DR TIGRFAMs; TIGR00302; TIGR00302;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 79 AA; 8551 MW; 2213A7E552E6F648 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DLDA 4
Db 45 DLDA 48

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SQ SEQUENCE 79 AA; 9201 MW; C391948F6C51FD98 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
DB 8 DLDA 11

RESULT 45

Q9LB27 PRELIMINARY; PRT; 80 AA.  
AC Q9LB27;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Chitinase A (EC 3.2.1.14) (fragment).  
GN CHIA.  
OS Chesapeake Bay isolate 6d.  
OC Bacteria; Proteobacteria; gamma subdivision.  
OX NCBI\_TaxID=116867;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=6D;  
RX PubMed=11053737;  
RA Ramaiah N., Hill R.T., Chun J., Ravel J., Matte M.H., Straube W.L.,  
RA Colwell R.R.;  
RT "Use of a chiA probe for detection of chitinase genes in bacteria from  
the Chesapeake Bay.";  
RL FEMS Microbiol. Ecol. 34:63-71(2000).  
DR EMBL; AF059504; AAF37590.1; -  
DR HSSP; P07254; ICTN.  
DR InterPro; IPR001223; Glyco\_hydro\_18.  
DR Pfam; PF00704; Glyco\_hydro\_18; 1.  
DR ProDom; PD000471; Glyco\_hydro\_18; 1.  
KW Glycosidase; Hydrolase.  
FT NON\_TER 1  
FT NON\_TER 80  
SQ SEQUENCE 80 AA; 8660 MW; 0F10CB9A71FAF84F CRC64;

Query Match 100.0%; Score 20; DB 2; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
DB 39 DLDA 42

Search completed: February 6, 2003, 11:21:55  
Job time : 24.3333 secs

RESULT 43

Q9A0C1 PRELIMINARY; PRT; 79 AA.  
AC Q9A0C1;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Hypothetical protein SPY0841.  
GN SPY0841.  
OS Streptococcus pyogenes.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
OC Streptococcaceae; Streptococcus.  
OX NCBI\_TaxID=1314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;  
RX MEDLINE=21192684; PubMed=11296296;  
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savić G., Lyon K.,  
RA Primeaux C., Serate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
RA Xuan Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
RA Qian X., Clifton S.W., Roe B.A., McLaughlin R.;  
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
DR EMBL; AE006534; AAK33771.1; -  
DR InterPro; IPR004087; KH\_dom.  
DR Pfam; PF00013; KH-domain; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 79 AA; 8872 MW; 0B79DB868FB4A33C CRC64;

Query Match 100.0%; Score 20; DB 16; Length 79;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLDA 4  
|  
|  
|  
|  
DB 38 DLDA 41

RESULT 44

Q926P1 PRELIMINARY; PRT; 79 AA.  
AC Q926P1;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Hypothetical protein plii0011.  
GN plii0011.  
OS Listeria innocua.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Listeriaceae; Listeria.  
OX NCBI\_TaxID=1642;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CLIP 11262 / SEROVAR 6A;  
RX PubMed=11679669;  
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Baquero F., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapat G.,  
RA Madoeno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;  
RT "Comparative genomics of Listeria species.";  
RL Science 294:849-852(2001).  
DR EMBL; AL592102; CAC42009.1; -  
KW Plasmid; Hypothetical protein; Complete proteome.





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 6, 2003, 11:16:00 ; Search time 27.8333 Seconds  
(without alignments)  
19.150 Million cell updates/sec

Title: PAT943-3

Perfect score: 21

Sequence: 1 syda 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 687

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
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- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
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- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	5	ABB06577	Amyloid protein pr
2	21	100.0	10	ABB06548	Beta-secretase cle
3	21	100.0	12	AA132812	Vascular endotheli
4	21	100.0	12	AA140040	Anti-hIL12 antibody
5	21	100.0	13	AA139650	Anti-IL12 antibody
6	21	100.0	13	AA139682	Anti-IL12 antibody
7	21	100.0	22	AA140588	SH3-binding peptid
8	21	100.0	25	AA140032	Human I-kappa-B-al
9	21	100.0	36	AA140055	Hib OMP P1 peptide
10	21	100.0	43	AA140858	Escherichia coli c

11	21	100.0	43	23	AAU77652	C-terminus of chim
12	21	100.0	50	20	AAW78216	Human secreted pro
13	21	100.0	51	22	AAE08853	His-1c2 protein C-
14	21	100.0	51	23	AAU77647	C-terminus of chim
15	21	100.0	56	22	ABBI1755	Human nervous syst
16	21	100.0	57	23	ABP33003	Human ORF1976 prot
17	21	100.0	65	22	ABB28160	Human peptide #811
18	21	100.0	65	22	ABB28240	Human peptide #891
19	21	100.0	65	22	ABB33335	Peptide #841 encod
20	21	100.0	65	22	ABB33415	Peptide #921 encod
21	21	100.0	65	22	ABBA0153	Peptide #7659 enco
22	21	100.0	65	22	ABBI1875	Protein #794 encod
23	21	100.0	65	22	ABBI1874	Protein #793 encod
24	21	100.0	65	22	ABB24610	Protein #6609 enco
25	21	100.0	65	22	AA144200	Human brain expres
26	21	100.0	65	22	AA160918	Human brain expres
27	21	100.0	65	22	AA166514	Human bone marrow
28	21	100.0	65	22	AA166594	Human bone marrow
29	21	100.0	65	22	AA173603	Human bone marrow
30	21	100.0	65	22	AA14387	Peptide #821 encod
31	21	100.0	65	22	AA14467	Peptide #901 encod
32	21	100.0	65	22	AA120034	Peptide #6468 enco
33	21	100.0	65	22	AA14454	Human EST encoded
34	21	100.0	65	22	AA126800	Peptide #837 encod
35	21	100.0	65	22	AA133798	Peptide #917 encod
36	21	100.0	65	22	AA133798	Peptide #7835 enco
37	21	100.0	65	22	AA121114	Peptide #796 encod
38	21	100.0	65	22	AA121194	Peptide #876 encod
39	21	100.0	65	23	ABG36166	Human peptide enco
40	21	100.0	65	23	ABG36246	Human peptide enco
41	21	100.0	65	23	ABG43473	Human peptide enco
42	21	100.0	71	23	ABP05806	Human ORFX protein
43	21	100.0	74	22	ABB35040	Peptide #2546 enco
44	21	100.0	74	22	ABB35934	Peptide #3440 enco
45	21	100.0	74	22	ABB20450	Protein #2449 enco

## ALIGNMENTS

RESULT 1  
ABB06577  
ID ABB06577 standard; Peptide: 5 AA.  
XX ABB06577;  
AC ABB06577;  
XX 31-MAY-2002 (first entry)  
DT Amyloid protein precursor mutagenic peptide SEQ ID NO:178.

DE Beta-secretase: enzyme; cleavage site; amyloid protein precursor; APP;  
KW aspartyl protease; neuroprotective; nontropic; beta-secretase inhibitor;  
KW Alzheimer's disease.

XX Homo sapiens.

OS Synthetic.

XX WO200206306-A2.

PN 24-JAN-2002.

PD 19-JUL-2001; 2001WO-US23035.

PF 19-JUL-2000; 2000US-219795P.

PR 12-MAR-2001; 2001US-275251P.

XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;

PI Heinrichson RL;

XX WPI; 2002-216995/27.

PT Novel substrates for human aspartyl protease useful for identifying  
PT modulators of beta secretase activity of aspartyl protease for treating  
PT Alzheimer's disease

XX Example 8; Page 90; 188pp; English.

PS The present invention describes an isolated peptide (I) comprising a  
CC sequence of at least four amino acids, where the peptide is a substrate  
CC for conducting aspartyl protease assays. (I) has neuroprotective and  
CC nootropic activities, and can be used as an inhibitor of beta-secretase  
CC activity. A beta-secretase modulator from the present invention can be  
CC used for inhibiting beta-secretase activity in vivo, and in the  
CC manufacture of a medicament for the treatment of Alzheimer's disease.  
CC Pharmaceutical compositions from the present invention can be used for  
CC treating a disease or condition characterised by an abnormal beta-  
CC secretase activity. (I) is useful for identifying agents that modulate  
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful  
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and  
CC ABB06409 to ABB06593 represent sequences used in the exemplification  
CC of the present invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 21; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

|||||

2 SYDA 5

RESULT 2

ABB06548  
ID ABB06548 standard; Peptide; 10 AA.

AC ABB06548;

XX 31-MAY-2002 (first entry)

DE Beta-secretase cleavage site peptide SEQ ID NO:143.

XX Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;  
KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;  
KW Alzheimer's disease.

XX Homo sapiens.

OS Synthetic.

XX WO200206306-A2.

XX 24-JAN-2002.

XX 19-JUL-2001; 2001WO-US23035.

XX 19-JUL-2000; 2000US-219795P.

PR 12-MAR-2001; 2001US-275251P.

XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;  
PI Heinrichson RL;

XX WPI; 2002-216995/27.

XX Novel substrates for human aspartyl protease useful for identifying  
PT modulators of beta secretase activity of aspartyl protease for treating  
PT Alzheimer's disease

XX Claim 20; Page 169; 188pp; English.

XX The present invention describes an isolated peptide (I) comprising a  
CC sequence of at least four amino acids, where the peptide is a substrate

CC for conducting aspartyl protease assays. (I) has neuroprotective and  
CC nootropic activities, and can be used as an inhibitor of beta-secretase  
CC activity. A beta-secretase modulator from the present invention can be  
CC used for inhibiting beta-secretase activity in vivo, and in the  
CC manufacture of a medicament for the treatment of Alzheimer's disease.  
CC Pharmaceutical compositions from the present invention can be used for  
CC treating a disease or condition characterised by an abnormal beta-  
CC secretase activity. (I) is useful for identifying agents that modulate  
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful  
CC as a core structure to construct derivatives. ABL49914 to ABL49925 and  
CC ABB06409 to ABB06593 represent sequences used in the exemplification  
CC of the present invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 21; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

|||||

4 SYDA 7

RESULT 3

AAV32812  
ID AAV32812 standard; peptide; 12 AA.

XX AAV32812;

XX 09-NOV-1999 (first entry)

XX Vascular endothelial growth factor receptor 3 polypeptide.

XX Signal transduction; proteolytic cleavage; renal tubular defect; uraemia;  
KW proteosome binding site; muscle wasting; eating disorder; AIDS;  
KW diabetes; Cushing's disease; growth hormone deficiency; inhibitor;  
KW ubiquitin; vascular endothelial growth factor receptor 3.

OS Synthetic.

XX EP943624-A1.

XX 22-SEP-1999.

XX 12-MAR-1998; 98EP-0200799.

XX 12-MAR-1998; 98EP-0200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

XX Controlling the availability and/or signal transduction capability  
PT of a cell surface receptor, useful for treating growth hormone  
PT deficiencies

PS Disclosure; Page 10; 36pp; English.

XX This sequence is a polypeptide from the vascular endothelial growth  
CC factor receptor 3. Sequences (AAV32794-Y32823) are examples of  
CC polypeptide sequences found at or near the ubiquitin/proteosome complex  
CC binding site located on the intracellular part of a cell surface  
CC receptor. These sequences are used in a method for controlling the  
CC availability and signal transduction capability of a cell surface  
CC receptor by administering an inhibitor that is capable of inhibiting  
CC proteolytic cleavage of the receptor. Inhibition of this proteolytic  
CC cleavage results in the receptors being present on the surface for longer  
CC and therefore signalling for longer to any hormones which might be  
CC increases the sensitivity of cells to any hormones which might be  
CC present. The inhibitor is either derived from, competes with or binds to  
CC a polypeptide sequence of which sequences AAV32794-Y32823 are examples.  
CC The inhibitor may be used to treat muscle wasting, associated with

CC disorders such as renal tubular defects, uraemia, diabetes, Cushing's  
 CC syndrome, cachexias, eating disorders, AIDS, after stress and during  
 CC neuromuscular disease.

XX Sequence 12 AA;

Query Match 100.0%; Score 21; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4  
 ||||  
 Db 9 SYDA 12

#### RESULT 4

AAB40040  
 ID AAB40040 standard; Peptide; 12 AA.

XX AAB40040;

XX 05-FEB-2001 (first entry)

XX Anti-hIL12 antibody light chain CDR3 amino acid sequence SEQ ID 556.

XX Human; neutralising antibody; Interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI ) BASF AG.

XX (GEMY ) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis -

XX Claim 32; Figure 2H; 377pp; English.

XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in  
 CC AAC61062-C61071. The antibody of the invention is a neutralising  
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;  
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;  
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.  
 CC The antibodies or antigen-binding fragments are useful in the treatment

CC of disorders associated with detrimental release of human IL-12,  
 CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.  
 CC They can also be used in the manufacture of a pharmaceutical composition  
 CC to treat human IL-12 disorders.

XX Sequence 12 AA;

Query Match 100.0%; Score 21; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4  
 ||||  
 Db 2 SYDA 5

#### RESULT 5

AAB39650

ID AAB39650 standard; Peptide; 13 AA.

XX AAB39650;

XX 05-FEB-2001 (first entry)

XX Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 166.

XX Human; neutralising antibody; Interleukin-12; IL-12; antiinflammatory;  
 KW complementarity determining region; CDR; antirheumatic; antiarthritic;  
 KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI ) BASF AG.

XX (GEMY ) GENETICS INST INC.

XX Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis -

XX Example 1; Page 127; 377pp; English.

XX This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in  
 CC AAC61062-C61071. The antibody of the invention is a neutralising  
 CC antibody and has antirheumatic; antiarthritic; antisclerotic;  
 CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;  
 CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.

CC The antibodies or antigen-binding fragments are useful in the treatment  
CC of disorders associated with detrimental release of human IL-12,  
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.  
CC They can also be used in the manufacture of a pharmaceutical composition  
CC to treat human IL-12 disorders.  
XX  
SQ

Sequence 13 AA;

Query Match 100.0%; Score 21; DB 21; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

||||

Db 2 SYDA 5

RESULT 6

AAB39682

ID AAB39682 standard; Peptide; 13 AA.

XX AAB39682;

XX 05-FEB-2001 (first entry)

DT Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 198.

DE Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;  
KW complementarity determining region; CDR; antirheumatic; antiarthritis;  
KW antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant;  
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

XX WO2000056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US07946.

XX 25-MAR-1999; 99US-0126603.

XX (BADI ) BASF AG.

XX (GEMY ) GENETICS INST INC.

XX Sajfield JG, Roguska M, Paskind M, Banerjee S, Tracey DF, White M;  
PI Kaynakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;  
PI Veldman GM, Venturini A, Warner NW, Widom A, Elvin JG, Duncan AR;  
PI Derbyshire EJ, Carmen S, Smith S, Holtet TL, Du Fou SL;

XX WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to  
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
PT disease and multiple sclerosis -

XX Example 1; Page 128; 377pp; English.

XX This invention relates to a new human antibody specific for human  
CC interleukin-12 (IL-12). The invention also includes antigen binding  
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
CC anti-IL-12 antibody heavy and light chain complementarity determining  
CC region (CDR) amino acid sequences, and also includes variable region  
CC amino acid sequences. Other variable region amino acid sequences are  
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
CC given in AAB40064-B40067. Primers used in the identification and  
CC construction of the antibodies of the invention are given in  
CC AAC61062-C61071. The antibody of the invention is a neutralising  
CC antibody and has antirheumatic; antiarthritis; antisclerotic;  
CC antiinflammatory; neuroprotective; antipsoriatic; antiasthmatic;

CC cardiant; antiparasitic; antibacterial and immunosuppressive activity.  
CC The antibodies or antigen-binding fragments are useful in the treatment  
CC of disorders associated with detrimental release of human IL-12,  
CC especially Crohn's disease, multiple sclerosis and rheumatoid arthritis.  
CC They can also be used in the manufacture of a pharmaceutical composition  
CC to treat human IL-12 disorders.  
XX  
SQ

Sequence 13 AA;

Query Match 100.0%; Score 21; DB 21; Length 13;

Best Local Similarity 100.0%; Pred. No. 63;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4

||||

Db 2 SYDA 5

RESULT 7

AAW05488

ID AAW05488 standard; Peptide; 22 AA.

XX AAW05488;

XX 24-FEB-1998 (first entry)

DE SH3-binding peptide P53PB2.P5.

XX Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;  
KW cellular signalling element; cellular structural element; malignancy;  
KW protein identification; functional domain; protein screening;  
KW cellular signal transduction process; binding peptide.

XX Synthetic.

XX WO9631625-A1.

XX 10-OCT-1996.

XX 04-APR-1996; 96WO-US04454.

XX 03-APR-1996; 96US-0630915.

XX 07-APR-1995; 95US-0417872.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;

XX WPI; 1996-465045/46.

XX Identifying polypeptide(s) having specific functional domain (esp.  
PT SH3 domain) - comprises detecting selective binding to recognition  
PT unit, regardless of sequence homology

XX Example; Fig 13; 174pp; English.

XX AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding  
CC peptides. These sequences were used as parts of multivalent recognition  
CC unit complexes used in the method of the invention. The method of the  
CC invention is for identifying polypeptides containing functional domains  
CC of interest (especially SH3 domains). It comprises contacting a  
CC multivalent recognition unit (RU) complex with a number of peptides and  
CC identifying polypeptides having a selective binding affinity for the RU  
CC complex. The method is based on functional similarities and does not  
CC rely on sequence similarities. Prior methods only gave limited success  
CC for identifying proteins containing an SH3 domain due to the minimal  
CC sequence homology among known SH3 proteins. Multivalent RU complexes are  
CC particularly suited to screening for polypeptides containing functional  
CC domains that are similar to, but not identical in sequence to, the  
CC original target functional domain. The new method enables proteins  
CC having a common function to be identified. Identification of novel SH3  
CC proteins will be useful for a better understanding of cell growth,

CC malignancy, signal transduction processes, etc. New candidate drugs can  
 CC be identified, and their specificities (e.g. pharmacological activities)  
 CC can be assessed using the method of the invention.

SQ Sequence 22 AA;

Query Match 100.0%; Score 21; DB 17; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4  
 ||||  
 Db 1 SYDA 4

## RESULT 8

AAW00324  
 ID AAW00324 standard; peptide; 25 AA.

AC AAW00324;

DT 23-JUN-1997 (first entry)

DE Human I-kappa-B-alpha residues 279-303, variant Thr291Ala.

XX Human; I-kappa-B-alpha; transcription factor; inhibitor; variant;  
 KW inhibition; suppression; phosphorylation; antiinflammation;  
 KW immunosuppression; antiinflammatory; immunosuppressant; mutant.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 13 /note= "wild type Thr substituted with Ala"

XX WO9632412-Al.

XX 17-OCT-1996.

XX 12-APR-1996; 96WO-JP01028.

XX 13-APR-1995; 95JP-0111033.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX (CHUS ) CHUGAI PHARM CO LTD.

XX Ishikawa Y, Kuno K, Matsushima K;

XX WPI; 1996-477071/47.

XX Peptide(s) which suppress the phosphorylation of I-kappa-B-alpha -  
 PT act as effective antiinflammatory and immunosuppressant agents

XX Example 1; Page 29; 43pp; Japanese.

XX The present peptide, which comprises residues 279-303 of human  
 CC I-kappa-B-alpha (a transcription factor inhibitor) and the mutation  
 CC Thr291Ala, suppresses I-kappa-B-alpha phosphorylation. It can be  
 CC used as an antiinflammatory or immunosuppressant, at a preferred  
 CC dosage of 0.001-1000 (particularly 0.01-10) mg/day orally or  
 CC non-orally.

SQ Sequence 25 AA;

Query Match 100.0%; Score 21; DB 17; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4  
 ||||  
 Db 10 SYDA 13

## RESULT 9

AAW00055

ID AAW00055 standard; peptide; 36 AA.

XX AAW00055;

XX 04-FEB-1994 (first entry)

XX Hib OMP P1 peptide HIBP1-3 (103-137).

XX Haemophilus influenzae; type b; Hib; outer membrane protein; P1; P2;  
 KW P6; vaccine; antibody; detection; lipoglycopeptide conjugate;  
 KW immunogen.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "May be absent"

XX WO9315205-A.

XX 05-AUG-1993.

XX 03-FEB-1993; 93WO-CA00041.

XX 03-FEB-1992; 92GB-0002219.

XX (CONN-) CONNAUGHT LAB LTD.

XX Chong P, Kandil A, Klein MH, Sia C;

XX WPI; 1993-258681/32.

XX Synthetic Haemophilus influenzae conjugate vaccine - comprising  
 PT T-helper cell determinants and B-cell epitope(s) linked to  
 PT synthetic oligo:saccharide(s)

XX Table 1; Page 47; 99pp; English.

XX The sequences given in AAW0053-101 are peptide fragments derived from  
 CC the Haemophilus influenzae type b (Hib) outer membrane proteins P1,  
 CC P2 and P6. These peptides may be used in a vaccine against Hib  
 CC infection and antibodies against these peptides may be used in test  
 CC kits to detect H. influenzae in a sample. The vaccine may further  
 CC comprise an immunogenic or immunostimulatory molecule or the peptides  
 CC may be modified with lipids, or linked to synthetic PRP as synthetic  
 CC lipoglycopeptide conjugates to produce alternative vaccines.

SQ Sequence 36 AA;

Query Match 100.0%; Score 21; DB 14; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4  
 ||||  
 Db 25 SYDA 28

## RESULT 10

AAE08858

ID AAE08858 standard; peptide; 43 AA.

XX AAE08858;

XX 15-NOV-2001 (first entry)

XX Escherichia coli chimeric CspA protein C-terminal peptide 1c2.

XX Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;  
 KW washing powder; cold shock protein; CspA.

OS Chimeric - Escherichia coli.  
XX Chimeric - Unidentified.  
PN WO200157065-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 02-FEB-2001; 2001WO-GB00445.  
XX  
XX 03-FEB-2000; 2000GB-0002492.  
PR 04-FEB-2000; 2000US-0180326.  
PR 03-JUL-2000; 2000GB-0016346.  
PR 07-AUG-2000; 2000GB-0019362.  
XX  
XX (DIVE-) DIVERSYS LTD.  
XX  
XX Riechmann L, Winter G;  
PI  
XX  
XX WPI; 2001-529779/58.  
XX  
XX Chimeric folded protein domain derived from repertoire of chimeric  
PT proteins useful therapeutically, comprises two or more sequence  
PT segments derived from parent amino acid sequence that are  
PT non-homologous -  
XX  
XX Example 16; Page 47; 75pp; English.  
XX  
XX The invention relates to a chimeric folded protein domain derived from  
CC a repertoire of chimeric proteins. The chimeric protein comprises two or  
CC more sequence segments derived from parent amino acid sequence that are  
CC non-homologous. The chimeric protein is useful in vaccination against  
CC one or more of the amino acid sequences from which the chimera is  
CC derived, for administration to a human for therapeutic purposes, and for  
CC use in a commercial product to which humans are exposed. The chimeric  
CC protein is useful as improved enzyme inhibitors, and to avoid  
CC sensitisation in humans (for e.g. enzymes and washing powders). The  
CC present sequence is Escherichia coli cold shock protein (CspA)  
CC C-terminal peptide chimeric protein used in the exemplification of  
CC the invention.  
XX  
XX Sequence 43 AA;  
SQ  
  
Query Match 100.0%; Score 21; DB 22; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SYDA 4  
Db 17 SYDA 20  
|||||  
  
RESULT 11  
AAU77652  
ID AAU77652 standard; Peptide; 43 AA.  
XX  
XX AAU77652;  
AC  
XX  
XX 05-JUN-2002 (first entry)  
DT  
XX  
XX C-terminus of chimaeric protein 1c2.  
DE  
XX  
XX RhsD; chimaeric folded protein domain; 1c2; vaccine; asthma;  
KW proteolysis resistance.  
KW  
XX  
XX Escherichia coli.  
OS Synthetic.  
OS  
XX  
XX WO200212277-A2.  
PN  
XX  
XX 14-FEB-2002.  
PD  
XX  
XX 03-AUG-2001; 2001WO-GB03508.  
PF  
XX

PR 07-AUG-2000; 2000GB-0019362.  
PR 02-FEB-2001; 2001GB-0002678.  
XX  
XX (DIVE-) DIVERSYS LTD.  
PA  
XX  
XX Riechmann L, Winter G;  
PI  
XX  
XX WPI; 2002-257461/30.  
XX  
XX Novel chimaeric folded protein domain, useful in vaccination, is derived  
PT from a repertoire of chimaeric proteins and comprises two or more  
PT sequence segments derived from parent non-homologous sequences -  
XX  
XX Example 6; Page 61; 94pp; English.  
XX  
XX The invention relates to a chimaeric folded protein domain, when derived  
CC from a repertoire of chimaeric proteins comprises two or more sequence  
CC segments derived from parent amino acid sequences that are non-  
CC homologous. Also included are nucleic acids encoding the chimaeric  
CC protein domains and a method of producing the protein domains.  
CC Chimaeric proteins His-2f3 and His-1c2 were used for immunisation of a  
CC rabbit to analyse, if resulting antisera from the immunised animals are  
CC crossreactive with CspA. The animals were then challenged with an  
CC injection of folded cold shock protein (CspA) to see if a specific  
CC anti-CspA immune response involving T cell mediated help was  
CC established during immunisation. The analyses of the rabbit immune  
CC response showed, that immunisation with both 2f3 and 1c2 raised  
CC antisera highly reactive with their respective antigen as they bound  
CC phage displaying the chimaeric proteins strongly after the second, third  
CC and fourth vaccination. Crossreactivity with CspA was observed.  
CC The protein domain is useful in vaccination against parent proteins from  
CC which the chimera is derived, for administration to a human for  
CC therapeutic purposes and for use in commercial product to which humans  
CC are exposed. The protein domains are useful for treating asthma and in  
CC immunisation. The chimaeric folded protein domain is resistant to in vivo  
CC or in vitro proteolysis by protease enzymes and is not immunogenic or  
CC weakly immunogenic, and hence suitable for therapeutic purposes and to  
CC avoid sensitisation in humans. The present sequence is the C-terminus of  
CC a chimaeric folded protein domain of the invention based on E.coli RhsD.  
XX  
XX Sequence 43 AA;  
SQ  
  
Query Match 100.0%; Score 21; DB 23; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SYDA 4  
Db 17 SYDA 20  
|||||  
  
RESULT 12  
AAW78216  
ID AAW78216 standard; Protein; 50 AA.  
XX  
XX AAW78216;  
AC  
XX  
XX 13-APR-1999 (first entry)  
DT  
XX  
XX Human secreted protein encoded by gene 34 clone HTTCN24.  
DE  
XX  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KW developmental abnormality; foetal deficiency; blood; allergy; renal;  
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KW cognitive disorder; schizophrenia; prostate; osteoclast; thymus;  
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH

FT Misc-difference 50  
XX /label= unknown

PN W09856804-A1.

XX 17-DEC-1998.

XX 11-JUN-1998; 98WO-US12125.

XX 02-OCT-1997; 97US-0061060.

XX 13-JUN-1997; 97US-0049547.

XX 13-JUN-1997; 97US-0049548.

XX 13-JUN-1997; 97US-0049549.

XX 13-JUN-1997; 97US-0049550.

XX 13-JUN-1997; 97US-0049606.

XX 13-JUN-1997; 97US-0049607.

XX 13-JUN-1997; 97US-0049608.

XX 13-JUN-1997; 97US-0049609.

XX 13-JUN-1997; 97US-0049610.

XX 13-JUN-1997; 97US-0049611.

XX 13-JUN-1997; 97US-0050566.

XX 13-JUN-1997; 97US-0050901.

XX 13-JUN-1997; 97US-0052989.

XX 08-JUL-1997; 97US-0051919.

XX 18-AUG-1997; 97US-0055984.

XX 12-SEP-1997; 97US-0058665.

XX 12-SEP-1997; 97US-0058668.

XX 12-SEP-1997; 97US-0058669.

XX 12-SEP-1997; 97US-0058750.

XX 12-SEP-1997; 97US-0058971.

XX 12-SEP-1997; 97US-0058972.

XX 12-SEP-1997; 97US-0058975.

XX 02-OCT-1997; 97US-0060834.

XX 02-OCT-1997; 97US-0060841.

XX 02-OCT-1997; 97US-0060844.

XX 02-OCT-1997; 97US-0060865.

XX 02-OCT-1997; 97US-0061059.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;

XX Moore FA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;

XX Yu GL;

XX WPI; 1999-080881/07.

XX N-PSDB; AAX04401.

XX New isolated human genes and the secreted polypeptides they encode -

FT useful for diagnosis and treatment of e.g. cancers, neurological

XX disorders, immune diseases, inflammation or blood disorders

XX Claim 11; Page 314; 380pp; English.

XX This sequence represents a secreted human protein encoded by the gene

XX clone detailed in the descriptor line. The gene can be used to generate

XX fusion proteins by linking to the gene to a human immunoglobulin Fc

XX portion (e.g. AAX04302) for increasing the stability of the fused

XX protein as compared to the human protein only.

XX The invention relates to 86 novel genes and their fragments (nucleic

XX acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)

XX which are useful for preventing, treating or ameliorating medical

XX conditions e.g. by protein or gene therapy. Also, pathological

XX conditions can be diagnosed by determining the amount of the new

XX polypeptides in a sample or by determining the presence of mutations in

XX the new polynucleotides. Specific uses are described for each of the 86

XX polynucleotides, based on which tissues they are most highly expressed in

XX (see AAX04311 for described uses).

XX Sequence 50 AA;

XX Query Match 100.0%; Score 21; DB 20; Length 50;

XX Best Local Similarity 100.0%; Pred. No. 2.7e+02;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4

DB 22 SYDA 25

XX 1111

XX 15-NOV-2001 (first entry)

XX His-1c2 protein C-terminal peptide sequence.

XX Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;

XX washing powder; His-1c2.

XX Unidentified.

XX OS

XX PN

XX PD

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-GB00445.

XX 03-FEB-2000; 2000GB-0002492.

XX 04-FEB-2000; 2000US-0180326.

XX 03-JUL-2000; 2000GB-0016346.

XX 07-AUG-2000; 2000GB-0019362.

XX (DIVE-) DIVERSYS LTD.

XX Riechmann L, Winter G;

XX WPI; 2001-529779/58.

XX Chimeric folded protein domain derived from repertoire of chimeric

XX proteins useful therapeutically, comprises two or more sequence

XX segments derived from parent amino acid sequence that are

XX non-homologous -

XX Example 16; Page 46; 75pp; English.

XX The invention relates to a chimeric folded protein domain derived from

XX a repertoire of chimeric proteins. The chimeric protein comprises two or

XX more sequence segments derived from parent amino acid sequence that are

XX non-homologous. The chimeric protein is useful in vaccination against

XX one or more of the amino acid sequences from which the chimera is

XX derived, for administration to a human for therapeutic purposes, and for

XX use in a commercial product to which humans are exposed. The chimeric

XX protein is useful as improved enzyme inhibitors, and to avoid

XX sensitisation in humans (for e.g. enzymes and washing powders). The

XX present sequence is C-terminal peptide sequence of His-1c2 protein used

XX in the exemplification of the invention.

XX Sequence 51 AA;

XX Query Match 100.0%; Score 21; DB 22; Length 51;

XX Best Local Similarity 100.0%; Pred. No. 2.8e+02;

QY 1 SYDA 4

DB 22 SYDA 25

XX 1111

XX 15-NOV-2001 (first entry)

XX His-1c2 protein C-terminal peptide sequence.

XX Chimeric folded protein; vaccine; therapeutic; enzyme inhibitor;

XX washing powder; His-1c2.

XX Unidentified.

XX OS

XX PN

XX PD

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-GB00445.

XX 03-FEB-2000; 2000GB-0002492.

XX 04-FEB-2000; 2000US-0180326.

XX 03-JUL-2000; 2000GB-0016346.

XX 07-AUG-2000; 2000GB-0019362.

XX (DIVE-) DIVERSYS LTD.

XX Riechmann L, Winter G;

XX WPI; 2001-529779/58.

XX Chimeric folded protein domain derived from repertoire of chimeric

XX proteins useful therapeutically, comprises two or more sequence

XX segments derived from parent amino acid sequence that are

XX non-homologous -

XX Example 16; Page 46; 75pp; English.

XX The invention relates to a chimeric folded protein domain derived from

XX a repertoire of chimeric proteins. The chimeric protein comprises two or

XX more sequence segments derived from parent amino acid sequence that are

XX non-homologous. The chimeric protein is useful in vaccination against

XX one or more of the amino acid sequences from which the chimera is

XX derived, for administration to a human for therapeutic purposes, and for

XX use in a commercial product to which humans are exposed. The chimeric

XX protein is useful as improved enzyme inhibitors, and to avoid

XX sensitisation in humans (for e.g. enzymes and washing powders). The

XX present sequence is C-terminal peptide sequence of His-1c2 protein used

XX in the exemplification of the invention.

XX Sequence 51 AA;

XX Query Match 100.0%; Score 21; DB 22; Length 51;

XX Best Local Similarity 100.0%; Pred. No. 2.8e+02;

XX  
DT 05-JUN-2002 (first entry)  
XX  
DE C-terminus of chimaeric protein His-1c2.  
XX  
KW CspA; chimaeric folded protein domain; His-1c2;  
KW cold shock protein; vaccine; asthma; proteolysis resistance.  
XX  
OS Escherichia coli.  
OS Synthetic.  
XX  
PN WO200212277-A2.  
XX  
PD 14-FEB-2002.  
XX  
XX 03-AUG-2001; 2001WO-GB03508.  
XX  
PR 07-AUG-2000; 2000GB-0019362.  
PR 02-FEB-2001; 2001GB-0002678.  
XX  
XX (DIVE-) DIVERSYS LTD.  
XX  
XX Riechmann L, Winter G;  
PI  
XX  
DR WPI; 2002-257461/30.  
XX  
PT Novel chimaeric folded protein domain, useful in vaccination, is derived  
PT from a repertoire of chimaeric proteins and comprises two or more  
PT sequence segments derived from parent non-homologous sequences -  
XX  
XX Example 4; Page 60; 94pp; English.  
XX  
CC The invention relates to a chimaeric folded protein domain, when derived  
CC from a repertoire of chimaeric proteins comprises two or more sequence  
CC segments derived from parent amino acid sequences that are non-  
CC homologous. Also included are nucleic acids encoding the chimaeric  
CC protein domains and a method of producing the protein domains.  
CC Chimaeric proteins His-2f3 and His-1c2 were used for immunisation of a  
CC rabbit to analyse, if resulting antisera from the immunised animals are  
CC crossreactive with CspA. The animals were then challenged with an  
CC injection of folded cold shock protein (CspA) to see if a specific  
CC anti-CspA immune response involving T cell mediated help was  
CC established during immunisation. The analyses of the rabbit immune  
CC response showed, that immunisation with both 2f3 and 1c2 raised  
CC antisera highly reactive with their respective antigen as they bound  
CC phage displaying the chimaeric proteins strongly after the second, third  
CC and fourth vaccination. Crossreactivity with CspA was observed.  
CC The protein domain is useful in vaccination against parent proteins from  
CC which the chimaera is derived, for administration to a human for  
CC therapeutic purposes and for use in commercial product to which humans  
CC are exposed. The protein domains are useful for treating asthma and in  
CC immunisation. The chimaeric folded protein domain is resistant to in vivo  
CC or in vitro proteolysis by protease enzymes and is not immunogenic or  
CC weakly immunogenic, and hence suitable for therapeutic purposes and to  
CC avoid sensitisation in humans. The present sequence is the C-terminus of  
CC a chimaeric folded protein domain, of the invention based on E.coli CspA.  
XX  
SQ Sequence 51 AA;  
Query Match 100.0%; Score 21; DB 23; Length 51;  
Best Local Similarity 100.0%; Preq. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 20 SYDA 23  
|||||  
RESULT 15  
ABB17155  
ID ABB17155 standard; Protein; 56 AA.  
XX  
AC ABB17155;

XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Human nervous system related polypeptide SEQ ID NO 5812.  
XX  
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
KW antiparkinsonian; antistickling; antianaemic; antiarthritic; cancer;  
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200159063-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01334.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0218880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 06-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.



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PR 14-SEP-2000; 2000US-0232399.  
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PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 20-OCT-2000; 2000US-0242221.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
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PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
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PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250391.  
PR 01-DEC-2000; 2000US-0251160.

PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251858.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-541565/60.  
XX N-PSDB; ABA13481.  
XX  
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating nervous system  
XX cancers and metastases -  
XX  
XX Claim 11; SEQ ID NO 5812; 1701pp + Sequence Listing; English.  
XX  
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins  
XX (AB14678-AB18001) useful for preventing, treating or ameliorating  
XX medical conditions e.g. by protein or gene therapy. The genes are  
XX isolated from a range of human tissues disclosed in the specification.  
XX The nucleic acids, proteins, antibodies and (ant)agonists are useful  
XX in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast  
XX and ovarian cancer and other cancers of the adrenal gland, bone, bone  
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
XX colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
XX and parasitic infections  
XX  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 56 AA;  
  
Query Match 100.0%; Score 21; DB 22; Length 56;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SYDA 4  
Db 27 SYDA 30  
|||||  
  
RESULT 16  
ABP33003  
ID ABP33003 standard; Protein; 57 AA.  
XX  
XX ABP33003;  
XX  
XX  
DT 08-JUL-2002 (first entry)  
XX  
DE Human ORF1976 protein, SEQ ID NO:3952.  
XX  
XX Human; ORF; open reading frame; ORF; drug screening; diagnosis;  
XX disease monitoring; cytokine; cell proliferation; cell differentiation;  
XX immune modulation; haematopoiesis regulation; tissue growth;  
XX angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;  
XX thrombolytic; tumour inhibition; bodily characteristic; fertility;  
XX behaviour; cancer; proliferative disorder; neurological disorder;  
XX cardiovascular disease; immune system disorder; organ transplantation;  
XX tissue growth disorder; tissue regeneration disorder; diabetes mellitus;

KW hypothyroidism; cholesterol ester storage disease; infection; vulneryary;  
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;  
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;  
KW cardiant; hypotensive; antihypertoid; antiinflammatory; immunomodulator;  
KW dermatological; analgesic; virucide; antibacterial; fungicide.  
XX  
OS Homo sapiens.  
XX  
XX WO200190366-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17076.  
PF  
XX  
XX 24-MAY-2000; 2000US-206690P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Leach MD, Shinkets RA;  
PI  
XX WPI; 2002-106200/14.  
DR N-PSDB; ABN77029.  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and disorders related to organ  
PT transplantation -  
XX  
XX Claim 10; Page 1246; 2508pp; English.  
XX  
XX Sequences ABP31028-ABP3561 represent 4534 novel human proteins  
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-  
CC ABN79587 represent cDNAs encoding them. The invention also encompasses  
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively  
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to  
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX  
CC polynucleotides, the recombinant production of ORFX proteins, antibodies  
CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and  
CC polypeptides, methods of screening for modulators of ORFX expression or  
CC activity, and methods of screening individuals for a predisposition to an  
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide  
CC range of biological activities, such as cytokine, cell proliferation,  
CC cell differentiation, immune modulation, haematopoiesis regulation,  
CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/  
CC chemokinetic activity, haemostatic activity, thrombolytic activity,  
CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,  
CC and antineoplastic activity, and may also be involved in the determination  
CC of bodily characteristics, fertility and behaviour. ORFX proteins,  
CC nucleic acids and antibodies may be used in the treatment of cancers,  
CC other proliferative disorders such as psoriasis and benign tumours,  
CC neurological disorders such as epilepsy and Alzheimer's disease,  
CC cardiovascular diseases, immune system disorders, disorders related to  
CC organ transplantation, disorders of tissue growth and regeneration,  
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester  
CC storage disease, and infectious diseases caused by viral, bacterial,  
CC fungal and other pathogens. ORFX nucleic acids may also be used as a  
CC source of primers and probes, in the detection of ORFX genomic sequences  
CC or transcripts, in the identification and cloning of homologous  
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX  
CC nucleic acids may additionally be used to produce transgenic animals  
CC which may be useful for studying the function and/or activity of ORFX  
CC protein, and in drug screening. The ORFX proteins may also be used as  
CC immunogens to generate specific antibodies, which are useful in the  
CC diagnosis, treatment and monitoring of ORFX-associated diseases.  
XX  
SQ Sequence 57 AA;

Query Match 100.0%; Score 21; DB 23; Length 57;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SYDA 4  
|||||

Db 8 SYDA 11  
RESULT 17  
ABB28160  
ID ABB28160 standard; Peptide; 65 AA.  
XX  
XX ABB28160;  
AC  
XX 01-FEB-2002 (first entry)  
DT  
XX  
DE Human peptide #811 encoded by breast cell single exon nucleic acid probe.  
XX  
XX Human; microarray; single exon probe; gene expression; breast;  
KW disease; cancer.  
KW  
XX Homo sapiens.  
OS  
XX WO200157271-A2.  
PN  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US00662.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR  
XX 26-MAY-2000; 2000US-0207456.  
PR  
XX 30-JUN-2000; 2000US-0608408.  
PR  
XX 03-AUG-2000; 2000US-0632366.  
PR  
XX 21-SEP-2000; 2000US-0234687.  
PR  
XX 27-SEP-2000; 2000US-0236359.  
PR  
XX 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-496933/54.  
DR  
XX  
XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX  
XX Claim 27; SEQ ID NO 11128; 327pp + sequence listing; English.  
PS  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting  
CC the probes with a collection of detectably labelled nucleic acids  
CC derived from mRNA of human breast, and then measuring the label  
CC bound to each probe of the microarray. The probes are useful for  
CC verifying the expression of regions of genomic DNA predicted to  
CC encode proteins. They are useful for gene discovery, and for  
CC determining predisposition and/or prognosing breast disease. Gene  
CC expression analysis is useful for assessing the toxicity of chemical  
CC agents on cells. The microarray of this invention presents a far greater  
CC diversity of probes for measuring gene expression, with far less bias  
CC than expressed sequence tag microarrays. The method is suitable for  
CC rapid production of functional information from genomic sequence. The  
CC present sequence is a peptide encoded by a single exon nucleic acid  
CC probe of the invention  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.  
XX  
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SYDA 4  
|||||  
Db 28 SYDA 31

RESULT 18  
ABB28240  
ID ABB28240 standard; Peptide; 65 AA.  
XX AC ABB28240;  
XX DT 01-FEB-2002 (first entry)  
XX DE Human peptide #891 encoded by breast cell single exon nucleic acid probe.  
XX DE Human; microarray; single exon probe; gene expression; breast;  
KW disease; cancer.  
XX OS Homo sapiens.  
XX PN WO200157271-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US00662.  
XX PR 04-FEB-2000; 2000US-0180312.  
XX PR 26-MAY-2000; 2000US-0207456.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234687.  
XX PR 27-SEP-2000; 2000US-0236359.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-496933/54.  
XX  
XX New spatially-addressable set of single exon nucleic acid probes,  
PT useful for measuring gene expression in sample derived from human  
PT breast, comprises number of single exon nucleic acid probes -  
XX  
XX Claim 27; SEQ ID NO 11208; 327pp + sequence listing; English.  
XX  
XX The invention relates to a spatially-addressable set of single exon  
XX nucleic acid probes for measuring gene expression in a sample derived  
XX from human breast and BT 474 cells. The method involves contacting  
XX the probes with a collection of detectably labelled nucleic acids  
XX derived from mRNA of human breast, and then measuring the label  
XX bound to each probe of the microarray. The probes are useful for  
XX verifying the expression of regions of genomic DNA predicted to  
XX encode proteins. They are useful for gene discovery, and for  
XX determining predisposition and/or prognosing breast disease. Gene  
XX expression analysis is useful for assessing the toxicity of chemical  
XX agents on cells. The microarray of this invention presents a far greater  
XX diversity of probes for measuring gene expression, with far less bias  
XX than expressed sequence tag microarrays. The method is suitable for  
XX rapid production of functional information from genomic sequence. The  
XX present sequence is a peptide encoded by a single exon nucleic acid  
XX probe of the invention.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 65 AA;  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDA 4  
|||||  
Db 36 SYDA 39

RESULT 19  
ABB33335  
ID ABB33335 standard; Peptide; 65 AA.  
XX AC ABB33335;  
XX DT 04-FEB-2002 (first entry)  
XX DE Peptide #841 encoded by human foetal liver single exon probe.  
XX DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX OS Homo sapiens.  
XX PN WO200157277-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US00669.  
XX PR 04-FEB-2000; 2000US-0180312.  
XX PR 26-MAY-2000; 2000US-0207456.  
XX PR 30-JUN-2000; 2000US-0608408.  
XX PR 03-AUG-2000; 2000US-0632366.  
XX PR 21-SEP-2000; 2000US-0234687.  
XX PR 27-SEP-2000; 2000US-0236359.  
XX PR 04-OCT-2000; 2000GB-0024263.  
XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
XX Claim 27; SEQ ID NO 25970; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
XX measuring human gene expression in a sample derived from human foetal  
XX liver. The single exon nucleic acid probes may be used for predicting,  
XX measuring and displaying gene expression in samples derived from human  
XX fetal liver. The present sequence is a peptide encoded by a single exon  
XX nucleic acid probe of the invention.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 65 AA;  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDA 4  
|||||  
Db 28 SYDA 31

RESULT 20  
ABB33415  
ID ABB33415 standard; Peptide; 65 AA.  
XX AC ABB33415;  
XX DT 04-FEB-2002 (first entry)  
XX DE Peptide #921 encoded by human foetal liver single exon probe.  
XX DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
KW Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX

OS Homo sapiens.  
PN WO200157277-A2.  
XX  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00669.  
PF  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
XX Claim 27; SEQ ID NO 26050; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 65 AA;  
SQ  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 36 SYDA 39  
RESULT 21  
ABB40153  
ID ABB40153 standard; Peptide; 65 AA.  
XX  
XX ABB40153;  
AC  
XX  
XX 04-FEB-2002 (first entry)  
DT  
XX  
DE Peptide #7659 encoded by human foetal liver single exon probe.  
XX  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
XX Homo sapiens.  
XX  
XX WO200157277-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US00669.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver -  
XX  
XX Claim 27; SEQ ID NO 32788; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 65 AA;  
SQ  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 22 SYDA 25  
RESULT 22  
ABB18795  
ID ABB18795 standard; Protein; 65 AA.  
XX  
XX ABB18795;  
AC  
XX  
XX 23-JAN-2002 (first entry)  
DT  
XX  
DE Protein #794 encoded by probe for measuring heart cell gene expression.  
XX  
XX Human; gene expression; heart; microarray; vascular system;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200157274-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US00666.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488899/53.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -

XX Claim 15; SEQ ID No 20565; 530pp; English.  
XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 65 AA;  
SQ Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 28 SYDA 31  
|||||  
RESULT 23  
ID ABB18874 standard; Protein; 65 AA.  
XX ABB18874;  
XX 23-JAN-2002 (first entry)  
DE Protein #873 encoded by probe for measuring heart cell gene expression.  
XX Human: gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
OS Homo sapiens.  
XX WO200157274-A2.  
PN 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US00666.  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488899/53.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX Claim 15; SEQ ID No 20644; 530pp; English.  
XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
XX PS

CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 65 AA;  
SQ Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 36 SYDA 39  
|||||  
RESULT 24  
ID ABB24610 standard; Protein; 65 AA.  
XX ABB24610;  
XX 23-JAN-2002 (first entry)  
DE Protein #669 encoded by probe for measuring heart cell gene expression.  
XX Human: gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
OS Homo sapiens.  
XX WO200157274-A2.  
PN 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US00666.  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488899/53.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX Claim 15; SEQ ID No 26380; 530pp; English.  
XX The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX

```
SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 25
AAM54200
ID AAM54200 standard; Protein; 65 AA.
XX AC
XX AC AAM54200;
XX AC
XX AC
DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 26305.
DE Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX Homo sapiens.
XX OS
XX WO200157275-A2.
XX PN
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00667.
XX PR
XX 04-FEB-2000; 2000US-0180312.
XX PR
XX 26-MAY-2000; 2000US-0207456.
XX PR
XX 30-JUN-2000; 2000US-0608408.
XX PR
XX 03-AUG-2000; 2000US-0632366.
XX PR
XX 21-SEP-2000; 2000US-0234687.
XX PR
XX 27-SEP-2000; 2000US-0236359.
XX PR
XX 04-OCT-2000; 2000GB-0024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 26305; 650pp + Sequence Listing; English.
XX CC
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 36 SYDA 39

RESULT 26
AAM60918
ID AAM60918 standard; Protein; 65 AA.
XX AC
XX AC AAM60918;
XX AC
XX AC
DT 05-NOV-2001 (first entry)
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 33023.
DE Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer.
XX Homo sapiens.
XX OS
XX WO200157275-A2.
XX PN
XX PD
XX 09-AUG-2001.
XX PF
XX 30-JAN-2001; 2001WO-US00667.
XX PR
XX 04-FEB-2000; 2000US-0180312.
XX PR
XX 26-MAY-2000; 2000US-0207456.
XX PR
XX 30-JUN-2000; 2000US-0608408.
XX PR
XX 03-AUG-2000; 2000US-0632366.
XX PR
XX 21-SEP-2000; 2000US-0234687.
XX PR
XX 27-SEP-2000; 2000US-0236359.
XX PR
XX 04-OCT-2000; 2000GB-0024263.
XX PA
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PI
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX DR
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX Example 4; SEQ ID NO: 26305; 650pp + Sequence Listing; English.
XX CC
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is a protein encoded by one of
XX the probes of the invention.
XX SQ Sequence 65 AA;
Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 27
AAM66514
ID AAM66514 standard; Protein; 65 AA.
XX AC
XX AC AAM66514;
XX AC
XX AC
DT 06-NOV-2001 (first entry)
XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26820.
DE Human; bone marrow expressed exon; gene expression analysis; probe;
XX microarray; cancer; leukaemia; lymphoma; myeloma.
XX Homo sapiens.
XX OS
XX OS
```

PN WO200157276-A2.  
 XX 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00668.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488900/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX Example 4; SEQ ID NO: 26820; 658pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX SQ Sequence 65 AA;  
 Query Match 100.0%; Score 21; DB 22; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SYDA 4  
 DB 28 SYDA 31  
 RESULT 28  
 AAM66594  
 ID AAM66594 standard; Protein; 65 AA.  
 AC AAM66594;  
 XX 06-NOV-2001 (first entry)  
 DT Human bone marrow expressed probe encoded protein SEQ ID NO: 26900.  
 DE Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 KW Homo sapiens.  
 OS  
 XX WO200157276-A2.  
 PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00668.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488900/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX Example 4; SEQ ID NO: 33909; 658pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488900/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX Example 4; SEQ ID NO: 26900; 658pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX SQ Sequence 65 AA;  
 Query Match 100.0%; Score 21; DB 22; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SYDA 4  
 DB 36 SYDA 39  
 RESULT 29  
 AAM73603  
 ID AAM73603 standard; Protein; 65 AA.  
 AC AAM73603;  
 XX 06-NOV-2001 (first entry)  
 DT Human bone marrow expressed probe encoded protein SEQ ID NO: 33909.  
 DE Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 KW Homo sapiens.  
 OS  
 XX WO200157276-A2.  
 PN 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US00668.  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488900/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 XX Example 4; SEQ ID NO: 33909; 658pp + Sequence Listing; English.  
 XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a

```
CC protein encoded by one of the probes of the invention.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 30
AAM14387
ID AAM14387 standard; Protein; 65 AA.
XX
AC AAM14387;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #821 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 19213; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||
Db 22 SYDA 25

RESULT 31
AAM14467
ID AAM14467 standard; Protein; 65 AA.
XX
AC AAM14467;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #901 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00670.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 19293; 487pp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 22; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4
    ||||
Db 36 SYDA 39

RESULT 32
AAM20034
ID AAM20034 standard; Protein; 65 AA.
XX
AC AAM20034;
XX
DT 12-OCT-2001 (first entry)
```



XX Peptide #6468 encoded by probe for measuring cervical gene expression.  
DE Probe: human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer.  
KW  
XX Homo sapiens.  
OS  
XX  
XX WO200157278-A2.  
PN  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00670.  
PF  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.  
XX 03-AUG-2000; 2000US-0632366.  
XX 21-SEP-2000; 2000US-0234687.  
XX 27-SEP-2000; 2000US-0236359.  
XX 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488901/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human cervical epithelial cells -  
XX  
XX Claim 27; SEQ ID No 24860; 487pp; English.  
PS  
XX The present invention relates to human single exon nucleic acid probes  
CC (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 65 AA;  
SQ  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 22 SYDA 25  
RESULT 33  
AAM24454  
ID AAM24454 standard; Protein; 65 AA.  
XX  
AC AAM24454;  
XX  
DT 12-OCT-2001 (first entry)  
DE  
XX Human EST encoded protein SEQ ID NO: 1979.  
XX  
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition.  
XX  
XX Homo sapiens.  
OS  
XX

PN WO200154477-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02687.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX  
DR WPI; 2001-476164/51.  
DR N-PSDB; AAH99113.  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
XX antibodies and research use -  
PS Claim 20; Page 1258-1259; 1275pp; English.  
XX  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention.  
XX  
XX Sequence 65 AA;  
SQ  
Query Match 100.0%; Score 21; DB 22; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SYDA 4  
Db 37 SYDA 40  
RESULT 34  
AAM26800  
ID AAM26800 standard; Protein; 65 AA.  
XX  
AC AAM26800;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #837 encoded by probe for measuring placental gene expression.  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
XX Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00663.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -  
 XX Claim 27; SEQ ID No 27069; 654pp; English.  
 XX The present invention relates to single exon nucleic acid probes (SENP:  
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.  
 XX  
 XX Sequence 65 AA;  
 SQ  
 Query Match 100.0%; Score 21; DB 22; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SYDA 4  
 Db 28 SYDA 31  
 ||||  
 RESULT 35  
 AAM26880  
 ID AAM26880 standard; Protein; 65 AA.  
 XX  
 AC AAM26880;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Peptide #917 encoded by probe for measuring placental gene expression.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00663.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -  
 XX Claim 27; SEQ ID No 27149; 654pp; English.  
 XX The present invention relates to single exon nucleic acid probes (SENP:  
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.  
 XX  
 XX Sequence 65 AA;  
 SQ  
 Query Match 100.0%; Score 21; DB 22; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SYDA 4  
 Db 36 SYDA 39  
 ||||  
 RESULT 36  
 AAM33798  
 ID AAM33798 standard; Protein; 65 AA.  
 XX  
 AC AAM33798;  
 XX  
 DT 17-OCT-2001 (first entry)  
 XX  
 DE Peptide #7835 encoded by probe for measuring placental gene expression.  
 XX  
 KW Probe; microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157272-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US00663.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488897/53.  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human placenta -  
 XX Claim 27; SEQ ID No 34067; 654pp; English.  
 XX The present invention relates to single exon nucleic acid probes (SENP:  
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders.  
 XX  
 XX Sequence 65 AA;  
 SQ  
 Query Match 100.0%; Score 21; DB 22; Length 65;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SYDA 4  
 Db 22 SYDA 25  
 ||||  
 RESULT 37



primary ciliary dyskinesia; pulmonary hypertension;  
hyaline membrane disease.

Homo sapiens.  
WO200186003-A2.  
15-NOV-2001.

30-JAN-2001; 2001WO-US000665.

04-FEB-2000; 2000US-180312P.  
26-MAY-2000; 2000US-207456P.  
30-JUN-2000; 2000US-0608408.  
03-AUG-2000; 2000US-0632366.  
21-SEP-2000; 2000US-234687P.  
27-SEP-2000; 2000US-236359P.  
04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to  
measure gene expression in human lung samples -

Claim 27; SEQ ID No 25831; 634pp; English.

The invention relates to a spatially-addressable set of single exon  
nucleic acid probes for measuring gene expression in a sample derived  
from human lung comprising single exon nucleic acid probes having one of  
12614 nucleic acid sequences mentioned in the specification, or their  
complements or the 12387 open reading frames derived from the 12614  
probes. Also included are a microarray comprising the novel set of  
probes; the novel set of probes which hybridise at high stringency to a  
nucleic acid expressed in the human lung; measuring gene expression in a  
sample derived from human lung, comprising (a) contacting the array with  
a collection of detectably labeled nucleic acids derived from human lung  
mRNA, and (b) measuring the label detectably bound to each probe of  
the array; identifying exons in a eukaryotic genome, comprising  
(a) algorithmically predicting at least one exon from genomic sequences  
of the eukaryote; and (b) detecting specific hybridisation of detectably  
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
having a fragment identical to the predicted exon, the probe is included  
in the above mentioned microarray; assigning exons to a single gene,  
comprising (a) identifying exons from genomic sequence by the method  
above and (b) measuring the expression of each of the exons in several  
tissues and/or cell types using hybridisation to a single exon  
microarrays having a probe with the exon, where a common pattern of  
expression of the exons in the tissues and/or cell types indicates that  
the exons should be assigned to a single gene; a peptide comprising one  
of 12011 sequences, mentioned in the specification, or encoded by the  
probes/open reading frames (ORF). The probes are used for gene  
expression analysis, and for identifying exons in a gene, particularly  
using human lung derived mRNA and for the study of lung diseases  
such as asthma, lung cancer, chronic obstructive pulmonary disease  
(COPD), interstitial lung disease (ILD), familial idiopathic pulmonary  
fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,  
Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary  
haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,  
pulmonary alveolar proteinosis, Karagenier syndrome, fibrocystic  
pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension  
and hyaline membrane disease. The present sequence is a peptide/protein  
encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part  
of the printed specification, but was obtained in electronic  
format directly from WIPO at  
ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;  
Best Local Similarity 100.0%; Pred. NO. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDA 4  
Db 28 SYDA 31

RESULT 40  
ABG36246  
ID ABG36246 standard; Peptide; 65 AA.

XX AC ABG36246;

XX DT 19-AUG-2002 (first entry)

XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 25911.

XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagenier syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.

XX OS Homo sapiens.

XX PN WO200186003-A2.

XX PD 15-NOV-2001.

XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-180312P.

XX PR 26-MAY-2000; 2000US-207456P.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-234687P.

XX PR 27-SEP-2000; 2000US-236359P.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2002-114183/15.

XX PT Spatially-addressable set of single exon nucleic acid probes, used to  
measure gene expression in human lung samples -

XX PS Claim 27; SEQ ID No 25911; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon  
nucleic acid probes for measuring gene expression in a sample derived  
from human lung comprising single exon nucleic acid probes having one of  
12614 nucleic acid sequences mentioned in the specification, or their  
complements or the 12387 open reading frames derived from the 12614  
probes. Also included are a microarray comprising the novel set of  
probes; the novel set of probes which hybridise at high stringency to a  
nucleic acid expressed in the human lung; measuring gene expression in a  
sample derived from human lung, comprising (a) contacting the array with  
a collection of detectably labeled nucleic acids derived from human lung  
mRNA, and (b) measuring the label detectably bound to each probe of  
the array; identifying exons in a eukaryotic genome, comprising  
(a) algorithmically predicting at least one exon from genomic sequences  
of the eukaryote; and (b) detecting specific hybridisation of detectably  
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
having a fragment identical to the predicted exon, the probe is included  
in the above mentioned microarray; assigning exons to a single gene,

comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4  
||||  
Db 36 SYDA 39

RESULT 41

ABG43473  
ID ABG43473 standard; Peptide; 65 AA.

AC ABG43473;

XX 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 33138.

KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.

OS Homo sapiens.

XX WO200186003-A2.

PN 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US00665.

XX 04-FEB-2000; 2000US-180312P.

PR 26-MAY-2000; 2000US-207456P.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-234687P.

PR 27-SEP-2000; 2000US-236359P.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -

PS Claim 27; SEQ ID No 33138; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 65 AA;

Query Match 100.0%; Score 21; DB 23; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDA 4  
||||  
Db 22 SYDA 25

RESULT 42

ABP05806

ID ABP05806 standard; Protein; 71 AA.

XX ABP05806;

AC ABP05806;

XX 24-JUN-2002 (first entry)

DE Human ORFX protein sequence SEQ ID NO:11594.

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

XX degenerative disorder; osteoarthritis; neurodegenerative disorder;  
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
XX hypertension; hypothyroidism; cholesterol ester storage disease;  
DE immune deficiency; immune disorder; infectious disease;  
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
KW myasthenia gravis.  
XX  
OS Homo sapiens.  
XX  
PN WO200192523-A2.  
XX  
PD 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US10836.  
XX  
XX 30-MAY-2000; 2000US-206132P.  
PR 29-AUG-2000; 2000US-228716P.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shinkets RA, Leach MD;  
XX  
XX WPI: 2002-106308/14.  
DR N-PSDB; ABN21558.  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
PT preventing and treating cardiovascular disease, neurodegenerative,  
PT hyperproliferative disorders and autoimmune disorders  
XX  
XX Disclosure; SEQ ID 11594; 1037pp; English.  
XX  
XX The present invention describes substantially purified human proteins  
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
CC treating or preventing a pathology associated with an ORFX-associated  
CC disorder in humans, and in the manufacture of a medicament for treating a  
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
CC sequences can be used in gene therapy. ORFX sequences can be used in the  
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,  
CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
CC storage disease, various immune deficiencies and disorders, infectious  
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
CC bone degenerative disorders, or periodontal disease, and for gut  
CC protection or regeneration and treatment of lung or liver fibrosis,  
CC reperfusion injury in various tissues and conditions resulting from  
CC systemic cytokine damage.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 71 AA;  
SQ  
Query Match 100.0%; Score 21; DB 23; Length 71;  
Best Local Similarity 100.0%; Pred. NO. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SYDA 4  
DB 6 SYDA 9  
RESULT 43  
ABB35040  
ID ABB35040 standard; Peptide; 74 AA.  
XX  
AC ABB35040;  
XX

XX 04-FEB-2002 (first entry)  
DT Peptide #2546 encoded by human foetal liver single exon probe.  
DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX Homo sapiens.  
XX WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00669.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI: 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver  
XX  
XX Claim 27; SEQ ID NO 27675; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 74 AA;  
SQ  
Query Match 100.0%; Score 21; DB 22; Length 74;  
Best Local Similarity 100.0%; Pred. NO. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SYDA 4  
DB 19 SYDA 22  
RESULT 44  
ABB35934  
ID ABB35934 standard; Peptide; 74 AA.  
XX  
XX ABB35934;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
XX Peptide #3440 encoded by human foetal liver single exon probe.  
DE Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX Homo sapiens.  
XX WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX